

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: June 1, 2005, 23:14:35 ; Search time 126.025 Seconds
(without alignments)
6151.841 Million cell updates/sec

Title: US-10-088-117A-18

Perfect score: 16

Sequence: 1 cbgayatcstrctgcc 16

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 4708233 seqs, 24227607955 residues

Total number of hits satisfying chosen parameters: 9416466

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 50 summaries

Database : GenEmbl.*

1: gb_ba.*

2: gb_hcg.*

3: gb_in.*

4: gb_om.*

5: gb_ov.*

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8: gb_pl.*

9: gb_pr.*

10: gb_ro.*

11: gb_sts.*

12: gb_sy.*

13: gb_un.*

14: gb_vi.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	14	87.5	16	AX098621	AX098621 Sequence
2	14	87.5	236	11 DM22G6T	Z50523 D. melanoga
3	14	87.5	594	6 BD163513	BD163513 Novel pol
4	14	87.5	594	6 AX121396	AX121396 Sequence
5	14	87.5	641	1 AX325561	AX325561 Unculture
6	14	87.5	641	1 AX325609	AX325609 Unculture
7	14	87.5	643	1 AX209024	AX209024 Unculture
8	14	87.5	643	1 AX209035	AX209035 Unculture
9	14	87.5	644	1 AX209099	AX209099 Unculture
10	14	87.5	644	1 AX325542	AX325542 Unculture
11	14	87.5	645	1 AX552337	AX552337 Unidentif
12	14	87.5	647	1 AX209048	AX209048 Unculture
13	14	87.5	647	1 AX209118	AX209118 Unculture
14	14	87.5	649	1 AX552386	AX552386 Unidentif
15	14	87.5	650	1 AX209084	AX209084 Unculture
16	14	87.5	650	1 AX325520	AX325520 Unculture
17	14	87.5	650	1 AX325522	AX325522 Unculture
18	14	87.5	650	1 AX325562	AX325562 Unculture
19	14	87.5	650	1 AX325585	AX325585 Unculture

20	14	87.5	650	1	AY453358	AY453358 Unculture
21	14	87.5	650	1	AY453363	AY453363 Unculture
22	14	87.5	650	1	AY453365	AY453365 Unculture
23	14	87.5	651	1	AY113837	AY113837 Unculture
24	14	87.5	651	1	AY552359	AY552359 Unidentif
25	14	87.5	651	1	AY552382	AY552382 Unidentif
26	14	87.5	652	1	AY113805	AY113805 Unculture
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31	14	87.5	652	1	AY552373	AY552373 Unidentif
32	14	87.5	653	1	AY113748	AY113748 Unculture
33	14	87.5	653	1	AY113776	AY113776 Unculture
34	14	87.5	653	1	AY113782	AY113782 Unculture
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36	14	87.5	653	1	AY209049	AY209049 Unculture
37	14	87.5	653	1	AY209050	AY209050 Unculture
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39	14	87.5	653	1	AY209058	AY209058 Unculture
40	14	87.5	653	1	AY209060	AY209060 Unculture
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44	14	87.5	653	1	AY209103	AY209103 Unculture
45	14	87.5	653	1	AY209108	AY209108 Unculture
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47	14	87.5	653	1	AY209120	AY209120 Unculture
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ALIGNMENTS

RESULT 1
AX098621
LOCUS AX098621 16 bp DNA linear PAT 02-APR-2001
DEFINITION Sequence 18 from Patent WO0120030.
ACCESSION AX098621
VERSION AX098621.1 GI:13537882
KEYWORDS synthetic construct
SOURCE synthetic construct
ORGANISM other sequences; artificial sequences.
REFERENCE 1
AUTHORS Giordano,G., dos Santos,J.P. and Mejean,V.
TITLE Nucleotide sequences derived from genes coding for trimethylamine n-oxide reductase, uses thereof in particular for detecting bacteria
JOURNAL Patent: WO 0120030-A 18 22-MAR-2001;
CENTRE NATIONAL DE LA RECHERCHE SCIENTIFIQUE (CNRS) (FR)
FEATURES
source
Location/Qualifiers
1..16
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="amorce PCR"

ORIGIN
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Best Local Similarity 100.0%; Pred. No. 3.3e+03; Indels 0; Gaps 0;
Matches 16; Conservative 0; Mismatches 0;
Oy 1 CBGAYATCSTRCTGCC 16
| | | | | | | | | | | | | | | |
Db 1 CBGAYATCSTRCTGCC 16

RESULT 2
DM22G6T/c
LOCUS DM22G6T 236 bp DNA linear STS 17-APR-1996

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OM nucleic - nucleic search, using sw model

Run on: June 1, 2005, 22:48:55 ; Search time 15.9815 Seconds
(without alignments)
5926.580 Million cell updates/sec

Title: US-10-088-117A-18

Perfect score: 16

Sequence: 1 cbgayatcstrtgcc 16

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 4390206 seqs, 2959870667 residues

Total number of hits satisfying chosen parameters: 8780412

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 50 summaries

Database : N_Geneseq_16Dec04:*

1: Geneseqn1980s:*

2: Geneseqn1990s:*

3: Geneseqn2000s:*

4: Geneseqn2001as:*

5: Geneseqn2001bs:*

6: Geneseqn2002as:*

7: Geneseqn2002bs:*

8: Geneseqn2003as:*

9: Geneseqn2003bs:*

10: Geneseqn2003cs:*

11: Geneseqn2003ds:*

12: Geneseqn2004as:*

13: Geneseqn2004bs:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
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4	14	87.5	741	12	Adi45730 Corn isop
5	14	87.5	741	12	AdJ44921 Plant cDN
6	14	87.5	883	13	AdS56043 Bacterial
7	14	87.5	1244	13	AdT05004 Haemophil
8	14	87.5	1470	11	AbD03667 Pseudomon
9	14	87.5	1563	11	AbD04037 Pseudomon
10	14	87.5	1896	12	AdM47884 Polynucle
11	14	87.5	1887	4	AaH19221 Human sec
12	14	87.5	1905	5	AaH79304 DNA encod
13	14	87.5	1956	13	AdS56469 Bacterial
14	14	87.5	2130	8	ACA31652 Prokaryot
15	14	87.5	2268	8	ACA31543 Prokaryot
16	14	87.5	2280	8	ACA50924 Prokaryot
17	14	87.5	2328	13	AdT45718 Bacterial
18	14	87.5	2358	8	ACA19185 Prokaryot
19	14	87.5	2358	13	AdS46037 Bacterial
20	14	87.5	2454	11	ACH97441 Klebsiell

21	14	87.5	2475	4	Aaf79948
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23	14	87.5	2503	4	Aaf71276
24	14	87.5	2544	4	Aaf79949
25	14	87.5	2547	13	AdS46046 Bacterial
26	14	87.5	2853	5	AaH72908 DNA encod
27	14	87.5	2853	5	AaH93061 DNA encod
28	14	87.5	2853	5	AaH92727 DNA encod
29	14	87.5	2853	5	AaH86655 DNA encod
30	14	87.5	3687	6	AdD28410 Bacillus
31	14	87.5	3687	13	AdT48591 Bacterial
32	14	87.5	3712	4	AaH19184 Human sec
33	14	87.5	3741	8	ACA35058 Prokaryot
34	14	87.5	3744	4	AaH56106 Salmoneil
35	14	87.5	3744	5	AaH66279 C glutami
36	14	87.5	3744	8	ACA51923 Prokaryot
37	14	87.5	3846	11	ACH97430 Klebsiell
38	14	87.5	3874	10	AdD13658 C. glutam
39	14	87.5	11275	6	AaH43717 E. coli g
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41	14	87.5	110000	2	Continuation (15 o
42	14	87.5	110000	6	ABA90521_14
43	14	87.5	22587	12	AdO97397 Human can
44	14	87.5	34980	5	AaH68528 C glutami
45	14	87.5	34980	13	AdT05648 Haemophil
46	13.2	82.5	277	3	AAC10817 Human sec
47	13.2	82.5	653	10	ACC73070 Human pan
48	13.2	82.5	763	2	AaH58279 DNA encod
49	13.2	82.5	972	5	AaH82875 DNA encod
50	13.2	82.5	998	5	AaH96227 Human bon

ALIGNMENTS

RESULT 1

AAF79957
ID AAF79957 standard; DNA; 16 BP.

AC AAF79957;

XX 11-JUN-2001 (first entry)

DE PCR primer used to amplify trimethylamine N-oxide reductase genes.

KW torA gene; trimethylamine N-oxide reductase; flesh degradation;

KW spoilage bacteria; fish; crustacean; PCR primer; ss.

OS Synthetic.

PN WO200120030-A2.

XX 22-MAR-2001.

PD 15-SEP-2000; 2000WO-FR002578.

XX 15-SEP-1999; 99FR-00011543.

XX (CNRS) CENT NAT RECH SCI.

XX Giordano G, Dos Santos J, Mejean V;

XX WPI; 2001-244822/25.

DR Detecting bacteria that cause flesh degradation in fish, for testing
XX freshness, comprises using probes or primers based on the trimethylamine
PT N-oxide reductase system.

XX Claim 7; Page 42; 9ipp; French.

CC PCR primers AAF79951-66 represent PCR primers used to amplify torA and
XX torC genes. TorA and torC are bacterial proteins of the trimethylamine N-
CC oxide reductase system. TorA nucleic acids are used for detecting, in a

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OM nucleic - nucleic search, using sw model

Run on: June 2, 2005, 08:20:11 ; Search time 4.94154 Seconds

(without alignments)
5298.032 Million cell updates/sec

Title: US-10-088-117A-18

Perfect score: 16

Sequence: 1 cbgayatcstrctgcc 16

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 1202784 seqs, 818138359 residues

Total number of hits satisfying chosen parameters: 2405568

Minimum DB seq length: 0

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Minimum DB seq length: 0
Maximum DB seq length: 2000000000
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Post-processing: Minimum Match 0%

Minimum Match 0%
Maximum Match 100%
Listing first 50 summaries

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4: /cgm2_6/pdata/1/ina/6B_COMB.seq.*
5: /cgm2_6/pdata/1/ina/PCTUS_COMB.seq.*
6: /cgm2_6/pdata/1/ina/backfiles1.seq.*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query		Length	DB	ID	Description
		Match	%				
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C 2	14	87.5	601	4	US-09-949-016-159206		Sequence 159206, A
C 3	14	87.5	1470	4	US-09-252-991A-2271		Sequence 2271, Ap
C 4	14	87.5	1563	4	US-09-252-991A-2641		Sequence 2641, Ap
C 5	14	87.5	2454	4	US-09-489-039A-3236		Sequence 3236, Ap
C 6	14	87.5	2503	4	US-09-602-777A-277		Sequence 277, App
7	14	87.5	3687	4	US-09-891-641-1		Sequence 1, Appli
8	14	87.5	3846	4	US-09-489-039A-3225		Sequence 3225, Ap
9	14	87.5	18157	4	US-09-949-016-16193		Sequence 16193, A
10	14	87.5	1830121	4	US-09-557-884-1		Sequence 1, Appli
11	14	87.5	1830121	4	US-09-643-990A-1		Sequence 1, Appli
C 12	13.2	82.5	277	4	US-09-513-999C-14892		Sequence 14892, A
C 13	13.2	82.5	368	4	US-09-621-976-30		Sequence 30, Appl
C 14	13.2	82.5	762	2	US-08-822-261-2		Sequence 2, Appli
C 15	13.2	82.5	762	4	US-09-226-852-2		Sequence 2, Appli
16	13.2	82.5	15853	4	US-09-949-016-12121		Sequence 12121, A
17	13.2	82.5	15853	4	US-09-949-016-16051		Sequence 16051, A
18	13	81.2	263	4	US-09-016-434-178		Sequence 178, App
C 19	13	81.2	351	4	US-09-270-767-4863		Sequence 4863, Ap
C 20	13	81.2	351	4	US-09-270-767-20145		Sequence 20145, A
21	13	81.2	416	4	US-09-544-398B-45		Sequence 45, Appl
22	13	81.2	416	4	US-09-543-771B-45		Sequence 45, Appl
C 23	13	81.2	440	2	US-08-318-837-2		Sequence 2, Appli
C 24	13	81.2	601	4	US-09-949-016-42148		Sequence 42148, A
25	13	81.2	699	4	US-09-902-540-5926		Sequence 5326, Ap
C 26	13	81.2	700	4	US-09-903-540-185		Sequence 185, App
27	13	81.2	780	3	US-08-990-823-70		Sequence 70, Appl

ALIGNMENTS

RESULT 1

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US-09-949-016-22155/c
; Sequence 22155, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOW
; TITLE OF INVENTION: WITH HUMAN DISEASE,
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-08-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 22155
; LENGTH: 601
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-22155

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Query Match 87.5%; Score 14; DB 4; Length 601;
Best Local Similarity 75.0%; Pred. No. 2e+02;
Matches 12; Conservative 4; Mismatches 0; Indels

Qy 1 CBGAYATCSTRCTGCC 16
 |::|::|::|::|::|
Db 63 CGGACATCCTGTCTGCC 48

RESULT 2

US-09-949-016-159206/c
; Sequence 159206, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14

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OM nucleic - nucleic search, using sw model

Run on: June 2, 2005, 16:25:53 ; Search time 17.0277 Seconds
(without alignments)
5776.400 Million cell updates/sec

Title: US-10-088-117A-18

Perfect score: 16

Sequence: 1 cbgayatcstrtgc 16

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 5706582 seqs, 3073711274 residues

Total number of hits satisfying chosen parameters: 11413164

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 50 summaries

Database : Published Applications NA:*

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- 4: /cgm2_6/ptodata/2/pubpna/US06_PUBCOMB.seq.*
- 5: /cgm2_6/ptodata/2/pubpna/US07_NEW_PUB.seq.*
- 6: /cgm2_6/ptodata/2/pubpna/PCTUS_PUBCOMB.seq.*
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- 21: /cgm2_6/ptodata/2/pubpna/US60_NEW_PUB.seq.*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	ID	Description
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6	14	87.5	811	18	US-10-425-115-42253
7	14	87.5	883	17	US-10-369-493-31717
8	14	87.5	1696	17	US-10-310-154-302
9	14	87.5	1696	19	US-10-732-923-246
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11	14	87.5	2130	17	US-10-282-122A-19522

12	14	87.5	2268	17	US-10-282-122A-19413
13	14	87.5	2280	17	US-10-282-122A-38794
14	14	87.5	2328	17	US-10-369-493-44156
15	14	87.5	2358	17	US-10-369-493-24467
16	14	87.5	2358	17	US-10-282-122A-7055
17	14	87.5	2547	17	US-10-369-493-24476
18	14	87.5	3687	9	US-09-891-641-1
19	14	87.5	3687	17	US-10-369-493-47029
20	14	87.5	3687	17	US-10-602-747A-1
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22	14	87.5	3741	17	US-10-282-122A-22928
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29	14	87.5	1830121	18	US-10-158-865-1
30	14	87.5	3309400	9	US-09-738-626-1
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32	13.2	82.5	712	13	US-10-027-632-16473
33	13.2	82.5	712	17	US-10-027-632-16473
34	13.2	82.5	762	15	US-10-316-761-2
35	13.2	82.5	3137	13	US-10-027-632-264695
36	13.2	82.5	3137	17	US-10-027-632-264695
37	13	81.2	25	19	US-10-719-900-37229
38	13	81.2	25	19	US-10-719-900-185408
39	13	81.2	47	14	US-10-013-173-16
40	13	81.2	47	15	US-10-150-762-16
41	13	81.2	47	15	US-10-244-821-16
42	13	81.2	141	18	US-10-425-115-95266
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44	13	81.2	192	15	US-10-156-761-5179
45	13	81.2	263	17	US-10-305-720-178
46	13	81.2	302	18	US-10-425-115-12070
47	13	81.2	359	9	US-09-917-800A-691
48	13	81.2	398	16	US-10-029-386-14441
49	13	81.2	401	9	US-09-864-761-32357
50	13	81.2	414	18	US-10-425-115-87116

ALIGNMENTS

RESULT 1

US-09-923-876-467
; Sequence 467, Application US/09923876
; Patent No. US20020013958A1
; GENERAL INFORMATION:
; APPLICANT: Lalqudi, Raghunath V.
; APPLICANT: Kamigaki, Laura Y. (Ito)
; APPLICANT: Sherman, Bradley K.
; TITLE OF INVENTION: POLYNUCLEOTIDES AND POLYPEPTIDES DERIVED FROM CORN SEEDLING
; FILE REFERENCE: PL-0012-1 CON
; CURRENT APPLICATION NUMBER: US/09/923,876
; CURRENT FILING DATE: 2001-08-06
; PRIOR APPLICATION NUMBER: 09/298,329
; PRIOR FILING DATE: 1999-04-21
; PRIOR APPLICATION NUMBER: 60/085,331
; PRIOR FILING DATE: 1998-05-05
; NUMBER OF SEQ ID NOS: 6332
; SOFTWARE: PERL Program
; SEQ ID NO 467
; LENGTH: 263
; TYPE: DNA
; ORGANISM: Zea mays
; FEATURE:
; NAME/KEY: misc feature
; OTHER INFORMATION: Incyte ID No. US20020013958A1 700156983H1
; US-09-923-876-467

Query Match 87.5%; Score 14; DB 9; Length 263;
Best Local Similarity 75.0%; Pred. No. 6.5e+02;

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OM nucleic - nucleic search, using sw model

Run on: June 2, 2005, 07:12:26 ; Search time 107.594 Seconds
(without alignments)
5660.438 Million cell updates/sec

Title: US-10-088-117A-18

Perfect score: 16

Sequence: 1 cbgayatcstrgtgc 16

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 34239544 seqs, 19032134700 residues

Total number of hits satisfying chosen parameters: 68479088

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 50 summaries

Database :

EST:*

1: gb_est1:*

2: gb_est2:*

3: gb_hic:*

4: gb_est3:*

5: gb_est4:*

6: gb_est5:*

7: gb_est6:*

8: gb_gss1:*

9: gb_gss2:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	14	87.5	188	9	CG733285
2	14	87.5	219	8	AZ868010
3	14	87.5	237	8	AZ857279
4	14	87.5	259	1	A1881564
5	14	87.5	328	8	AZ755055
6	14	87.5	363	7	W87131
7	14	87.5	365	4	BG837422
8	14	87.5	381	7	W11810
9	14	87.5	391	6	CD783767
10	14	87.5	408	5	BY298653
11	14	87.5	423	6	CD091125
12	14	87.5	459	8	BH240839
13	14	87.5	484	5	BZ266837
14	14	87.5	492	1	A4914387
15	14	87.5	513	8	B47814
16	14	87.5	529	8	AQ434937
17	14	87.5	537	6	CD793456
18	14	87.5	550	5	BP339064
19	14	87.5	570	9	CR205324
20	14	87.5	578	6	CB536706
21	14	87.5	586	6	CD780356
22	14	87.5	589	6	CD785404
23	14	87.5	594	7	CO531075
24	14	87.5	603	7	CO530140

25	14	87.5	611	6	CD793634
26	14	87.5	614	8	AQ418346
27	14	87.5	629	9	CNS03K21
28	14	87.5	636	4	BG859034
29	14	87.5	641	8	BH240856
30	14	87.5	643	9	CR836654
31	14	87.5	659	6	CD727887
32	14	87.5	663	1	AU171960
33	14	87.5	669	1	AU168386
34	14	87.5	676	8	BH240857
35	14	87.5	683	7	CV031060
36	14	87.5	687	5	BQ157381
37	14	87.5	694	8	BH240937
38	14	87.5	697	7	CO525966
39	14	87.5	698	9	CG108657
40	14	87.5	715	6	CD787450
41	14	87.5	729	6	CD787993
42	14	87.5	734	4	BQ709624
43	14	87.5	735	8	BH240782
44	14	87.5	738	7	CF698998
45	14	87.5	740	1	AJ801168
46	14	87.5	746	6	CD796273
47	14	87.5	756	6	CD780487
48	14	87.5	757	9	CG134378
49	14	87.5	764	5	BX926800
50	14	87.5	770	7	CO060110

ALIGNMENTS

CG733285 188 bp DNA linear GSS 20-OCT-2003
1119155C11.y1.1119 - RescueMu Grid AA Zea mays genomic, genomic
survey sequence.

CG733285
CG733285.1 GI:37775777

GSS:

Zea mays

ORGANISM

Zea mays

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD

clade; Panicoideae; Andropogoneae; Zea.

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

Maize genomic sequences found using engineered RescueMu transposon

Walbot,V.

Unpublished (2001)

Contact: Walbot V

Department of Biological Sciences

Stanford University,

855 California Ave, Palo Alto, CA 94304, USA

Tel: 650 723 2227

Fax: 650 725 8221

Email: walbot@stanford.edu

Plate: 1119155 row: 6

Class: transposon-tagged.

Location/Qualifiers

1. 188

/organism="Zea mays"

/mol_type="genomic DNA"

/cultivar="mixed background W23/A188/B73/K55"

/db_xref="taxon:4577"

/lab_host="adult"

/tissue_type="leaf"

/lab_host="DH10B"

/clone_lib="1119 - RescueMu Grid AA"

/notes="Organ: leaf; Vector: RescueMu (engineered from

pBluescript backbone); Site: 1: BamHI, Site: 2: BglII;

RescueMu is a 4.9 kb, modified maize Mu transposon

designed to allow plasmid rescue from total genomic DNA.

Mu elements insert preferentially into transcription

units. For more information on RescueMu, go to the web

GenCore version 5.1.6

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OM nucleic - nucleic search, using sw model

Run on: June 1, 2005, 23:14:35 ; Search time 157.531 Seconds

(without alignment)
6151.841 Million cell updates/sec

Title: US-10-088-117A-19

Perfect score: 20

Sequence: 1 ggmgaytaytcacmggygc 20

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 4708233 seqs, 24227607955 residues

Total number of hits satisfying chosen parameters: 9416466

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 50 summaries

Database :

GenEmbl.*
 1: gb_ba.*
 2: gb_hcg.*
 3: gb_in.*
 4: gb_om.*
 5: gb_ov.*
 6: gb_pat.*
 7: gb_ph.*
 8: gb_pi.*
 9: gb_pr.*
 10: gb_ro.*
 11: gb_sts.*
 12: gb_sy.*
 13: gb_un.*
 14: gb_vl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	17.2	86.0	20	6	AX098622
2	17.2	86.0	1998	6	AR387097
3	17.2	86.0	2385	6	AR387009
4	17.2	86.0	2475	6	AX098610
5	17.2	86.0	2486	6	AX098605
6	17.2	86.0	2487	6	AX098604
7	17.2	86.0	2487	6	AX098606
8	17.2	86.0	2490	1	SPU5974
9	17.2	86.0	2523	6	AX098609
10	17.2	86.0	2540	1	RCDSTNORG
11	17.2	86.0	2544	6	AX098612
12	17.2	86.0	3235	1	AF134212
13	17.2	86.0	4680	1	ECTOR
14	17.2	86.0	5637	1	RCU49506
15	17.2	86.0	6915	1	SNA6085
16	17.2	86.0	7990	1	AF018236
17	17.2	86.0	10726	1	AE015567
18	17.2	86.0	13067	1	AE015128
19	17.2	86.0	18252	1	D90737

20	17.2	86.0	19650	1	D90736
21	17.2	86.0	22072	1	AE008869
22	17.2	86.0	110000	1	U00096.10
23	17.2	86.0	190822	2	AC051613
24	17.2	86.0	265050	1	AL627281
25	17.2	86.0	272545	2	AC090533
26	17.2	86.0	292504	1	AE016981
27	17.2	86.0	300102	1	AE016981
28	17.2	86.0	301276	1	AE016758
29	17.2	86.0	302212	1	AE017147
30	16.4	82.0	21	6	AX098615
31	16.4	82.0	10968	1	AE004270
32	16.2	81.0	408	6	CQ442063
33	16	80.0	3337	1	ECOBISCASD
34	16	80.0	10593	1	AE015366
35	16	80.0	10715	1	AE006216
36	16	80.0	11006	1	AE005582
37	16	80.0	11289	1	AE005293
38	16	80.0	22418	1	AE008878
39	16	80.0	110000	1	U00096.37
40	16	80.0	154978	2	AC073952
41	16	80.0	173938	2	AC148536
42	16	80.0	200491	9	AC007249
43	16	-80.0	225419	1	ECUW76
44	16	80.0	245050	1	AL627280
45	16	80.0	267888	1	AP002565
46	16	80.0	289816	1	AE016992
47	16	80.0	299130	1	AP005077
48	16	80.0	300592	1	AE016846
49	16	80.0	301660	1	AE016768
50	16	80.0	327773	1	AP002554

ALIGNMENTS

RESULT 1
 AX098622

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

FEATURES

source

ORIGIN

Query Match

Best Local Similarity

Matches

Conservative

Mismatches

Indels

Gaps

Length

Score

Pred. No.

0;

0;

0;

0;

0;

0;

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0;

0;

0;

0;

0;

0;

0;

0;

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model
Run on: June 1, 2005, 22:48:55 ; Search time 19.9769 Seconds
(without alignments)
5926.580 Million cell updates/sec

Title: US-10-088-117a-19
Perfect score: 20
Sequence: 1 gmgaytactcagcmgygc 20

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 4390206 seqs, 2959870667 residues

Total number of hits satisfying chosen parameters: 8780412

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 50 summaries

- Database : N Geneseq_16Dec04.*
1: Geneseqn1980s.*
2: Geneseqn1990s.*
3: Geneseqn2000s.*
4: Geneseqn2001as.*
5: Geneseqn2001bs.*
6: Geneseqn2002as.*
7: Geneseqn2002bs.*
8: Geneseqn2003as.*
9: Geneseqn2003bs.*
10: Geneseqn2003cs.*
11: Geneseqn2003ds.*
12: Geneseqn2004as.*
13: Geneseqn2004bs.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	17.2	86.0	20	4	Aaf79958 PCR prime
2	17.2	86.0	1998	11	Ach98031 Klebsiell
3	17.2	86.0	2385	11	Ach97943 Klebsiell
4	17.2	86.0	2475	4	Aaf79948 Nucleotid
5	17.2	86.0	2486	4	Aaf79944 Nucleotid
6	17.2	86.0	2487	4	Aaf79945 Nucleotid
7	17.2	86.0	2487	4	Aaf79943 Nucleotid
8	17.2	86.0	2523	4	Aaf79947 Nucleotid
9	17.2	86.0	2544	4	Aaf79949 Nucleotid
10	17.2	86.0	2547	13	AdS46046 Bacterial
11	17.2	86.0	11275	6	Aah43717 E. coli 9
12	16.4	82.0	21	4	Aaf79951 PCR prime
13	16.2	81.0	408	6	Abn19673 Human ORF
14	16	80.0	1455	5	Aas86797 DNA encod
15	16	80.0	2220	13	AdT48846 Bacterial
16	15.6	78.0	780	11	Abd01207 Klebsiell
17	15.6	78.0	2120	13	AdS58851 Bacterial
18	15.6	78.0	2556	8	ACA38838
19	15.6	78.0	2637	12	AdL03795 DNA encod
20	15.6	78.0	2742	13	AdR85388 Aspergill

21	15.6	78.0	2809	13	ADR84801
22	15.6	78.0	8809	13	ADR84214
23	15.6	78.0	23210	4	AAF28530
24	15.2	76.0	1883	5	ABV23467
25	15.2	76.0	1883	5	ABV23113
26	15.2	76.0	1883	5	ABV29325
27	15.2	76.0	2448	13	ADS46130
28	15.2	76.0	7410	5	AAS74643
29	15.2	76.0	7410	5	AAS93051
30	15.2	76.0	10161	5	AAS93288
31	15	75.0	655	3	AAF07946
32	15	75.0	980	13	ADR62409
33	15	75.0	1435	13	ADR64626
34	15	75.0	3291	12	ADO00942
35	15	75.0	5404	4	ABL14953
36	15	75.0	12870	4	ABL14952
37	14.8	74.0	1242	5	AAH67611
38	14.8	74.0	34980	5	AAH68532
39	14.6	73.0	486	8	ABZ54835
40	14.6	73.0	523	5	ABV35656
41	14.6	73.0	523	5	ABV44461
42	14.6	73.0	595	13	ADR13125
43	14.6	73.0	617	13	ADR13124
44	14.6	73.0	782	5	ABV14577
45	14.6	73.0	988	6	ABL89972
46	14.6	73.0	1248	13	ADR13562
47	14.6	73.0	1542	10	ADB78939
48	14.6	73.0	2642	4	AAK94318
49	14.6	73.0	2642	12	ADL30960
50	14.6	73.0	2732	13	ADR08163

ALIGNMENTS

RESULT 1

AAF79958
ID AAF79958 standard; DNA; 20 BP.

XX
AC AAF79958;

XX
DT 11-JUN-2001 (first entry)

XX
DE PCR primer used to amplify trimethylamine N-oxide reductase genes.

XX
KW torA gene; trimethylamine N-oxide reductase; flesh degradation;

XX
KW spoilage bacteria; fish; crustacean; PCR primer; ss.

XX
OS Synthetic.

XX
PN WO200120030-A2.

XX
PD 22-MAR-2001.

XX
PF 15-SEP-2000; 2000WO-FR002578.

XX
PR 15-SEP-1999; 99FR-00011543.

XX
PA (CNRS) CENT NAT RECH SCI.

XX
PI Giordano G, Dos Santos J, Mejean V;

XX
DR WPI; 2001-244822/25.

XX
PT Detecting bacteria that cause flesh degradation in fish, for testing

XX
PT freshness, comprises using probes or primers based on the trimethylamine

XX
PS N-oxide reductase system.

XX
PS Claim 7; Page 42; 91pp; French.

XX
CC PCR primers AAF79951-66 represent PCR primers used to amplify torA and

XX
CC torC genes. TorA and torC are bacterial proteins of the trimethylamine N-

XX
CC oxide reductase system. TorA nucleic acids are used for detecting, in a

Result No.	Score	Query		Length	DB	ID	Description
		Match	%				
C 1	17.2	85.0	1998	4	US-09-489-039A-3826		Sequence 3826, Ap
C 2	17.2	78.0	2385	4	US-09-489-039A-3738		Sequence 3738, Ap
C 3	15.6	78.0	780	4	US-09-489-039A-6982		Sequence 6982, Ap
C 4	15.6	78.0	2637	4	US-09-540-236-1481		Sequence 1481, Ap
C 5	15.6	78.0	23210	4	US-09-596-002-137		Sequence 17, Appl
C 6	14.4	72.0	303	4	US-09-513-999C-11097		Sequence 11097, A
C 7	14.4	72.0	312	3	US-09-060-756-506		Sequence 506, App
C 8	14.4	72.0	312	4	US-09-670-314-506		Sequence 506, App
C 9	14.4	72.0	459	4	US-09-489-039A-6694		Sequence 6694, Ap
C 10	14.4	72.0	1752	4	US-09-489-039A-6747		Sequence 6747, Ap
C 11	14.4	72.0	82125	4	US-09-949-016-13517		Sequence 13517, A
C 12	14.4	72.0	82125	4	US-09-949-016-13518		Sequence 13518, A
C 13	14.4	72.0	135030	4	US-09-949-016-14896		Sequence 14896, A
C 14	14.4	72.0	251672	4	US-09-949-016-17926		Sequence 17296, A
C 15	14.4	72.0	251682	4	US-09-949-016-11973		Sequence 11973, A
C 16	14.4	72.0	4403765	3	US-09-103-840A-2		Sequence 2, Appl
C 17	14.4	72.0	4411529	3	US-09-103-840A-1		Sequence 1, Appl
C 18	14.2	71.0	2294	4	US-09-270-767-10469		Sequence 10469, A
C 19	14.2	71.0	1230025	4	US-09-198-452A-1		Sequence 1, Appl
C 20	14.2	71.0	1230230	4	US-09-438-185A-1		Sequence 1, Appl
C 21	14	70.0	93	3	US-08-952-793-269		Sequence 269, App
C 22	14	70.0	93	3	US-08-849-928-269		Sequence 269, App
C 23	14	70.0	93	5	PCT-US96-09455A-269		Sequence 269, App
C 24	14	70.0	281	4	US-09-513-999C-12276		Sequence 12276, A
C 25	14	70.0	458	4	US-09-270-767-12137		Sequence 12137, A
C 26	14	70.0	597	4	US-09-252-991A-8183		Sequence 8183, Ap
C 27	14	70.0	601	4	US-09-949-016-20773		Sequence 20773, A

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OM nucleic - nucleic search, using sw model

Run on: June 2, 2005, 16:25:53 ; Search time 21.2846 Seconds
(without alignments)
5776.400 Million cell updates/sec

Title: US-10-088-117A-19

Perfect score: 20

Sequence: 1 gmgaytaytcacmggygc 20

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 5706582 seqs, 3073711274 residues

Total number of hits satisfying chosen parameters: 11413164

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Listing first 50 summaries

Database :

Published Applications NA:**

- 1: /cgn2_6/ptodata/2/pubpna/US07_PUBCOMB.seq.*
- 2: /cgn2_6/ptodata/2/pubpna/PCT_NEW_PUB.seq.*
- 3: /cgn2_6/ptodata/2/pubpna/US06_NEW_PUB.seq.*
- 4: /cgn2_6/ptodata/2/pubpna/US06_PUBCOMB.seq.*
- 5: /cgn2_6/ptodata/2/pubpna/US07_NEW_PUB.seq.*
- 6: /cgn2_6/ptodata/2/pubpna/PCTUS_PUBCOMB.seq.*
- 7: /cgn2_6/ptodata/2/pubpna/US08_NEW_PUB.seq.*
- 8: /cgn2_6/ptodata/2/pubpna/US08_PUBCOMB.seq.*
- 9: /cgn2_6/ptodata/2/pubpna/US09A_PUBCOMB.seq.*
- 10: /cgn2_6/ptodata/2/pubpna/US09B_PUBCOMB.seq.*
- 11: /cgn2_6/ptodata/2/pubpna/US09C_PUBCOMB.seq.*
- 12: /cgn2_6/ptodata/2/pubpna/US09_NEW_PUB.seq.*
- 13: /cgn2_6/ptodata/2/pubpna/US10A_PUBCOMB.seq.*
- 14: /cgn2_6/ptodata/2/pubpna/US10B_PUBCOMB.seq.*
- 15: /cgn2_6/ptodata/2/pubpna/US10C_PUBCOMB.seq.*
- 16: /cgn2_6/ptodata/2/pubpna/US10D_PUBCOMB.seq.*
- 17: /cgn2_6/ptodata/2/pubpna/US10E_PUBCOMB.seq.*
- 18: /cgn2_6/ptodata/2/pubpna/US10F_PUBCOMB.seq.*
- 19: /cgn2_6/ptodata/2/pubpna/US10_NEW_PUB.seq.*
- 20: /cgn2_6/ptodata/2/pubpna/US11_NEW_PUB.seq.*
- 21: /cgn2_6/ptodata/2/pubpna/US60_NEW_PUB.seq.*
- 22: /cgn2_6/ptodata/2/pubpna/US60_PUBCOMB.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1.	17.2	86.0	2547	17	US-10-369-493-24476 Sequence 24476, A
2.	17.2	86.0	11275	16	US-10-240-689-39 Sequence 39, Appl
3.	16	80.0	2220	17	US-10-369-493-47284 Sequence 47284, A
4.	15.6	78.0	398	17	US-10-242-535A-21879 Sequence 21879, A
5.	15.6	78.0	398	17	US-10-085-783A-21879 Sequence 21879, A
6.	15.6	78.0	2120	17	US-10-369-493-34525 Sequence 34525, A
7.	15.6	78.0	2556	17	US-10-282-122A-26708 Sequence 26708, A
8.	15.6	78.0	3201	18	US-10-437-963-54673 Sequence 54673, A
9.	15.6	78.0	23210	17	US-10-672-787-17 Sequence 17, Appl
10	15.6	78.0	2731748	18	US-10-297-465A-1 Sequence 1, Appli
11	15.2	76.0	1883	18	US-10-357-930-23456 Sequence 23456, A

12	15.2	76.0	1883	18	US-10-357-930-23456
13	15.2	76.0	1883	18	US-10-357-930-23456
14	15.2	76.0	2448	17	US-10-369-493-24560
15	15	75.0	255	18	US-10-437-963-75824
16	15	75.0	655	18	US-10-653-047-469
17	15	75.0	980	18	US-10-767-795-3190
18	15	75.0	1435	18	US-10-767-795-5407
19	15	75.0	3291	17	US-10-263-929-80
20	14.8	74.0	1242	9	US-09-738-626-2646
21	14.8	74.0	3309400	9	US-09-738-626-1
22	14.6	73.0	314	18	US-10-425-115-3928
23	14.6	73.0	347	17	US-10-424-599-98600
24	14.6	73.0	359	18	US-10-425-115-184059
25	14.6	73.0	523	18	US-10-357-930-35674
26	14.6	73.0	523	18	US-10-357-930-44480
27	14.6	73.0	657	18	US-10-767-701-4589
28	14.6	73.0	668	18	US-10-425-115-178403
29	14.6	73.0	767	18	US-10-767-701-5491
30	14.6	73.0	776	13	US-10-027-632-32434
31	14.6	73.0	776	17	US-10-027-632-32434
32	14.6	73.0	782	18	US-10-357-930-14568
33	14.6	73.0	823	13	US-10-027-632-159760
34	14.6	73.0	823	13	US-10-027-632-159761
35	14.6	73.0	823	17	US-10-027-632-159761
36	14.6	73.0	823	17	US-10-027-632-159761
37	14.6	73.0	879	18	US-10-425-115-115730
38	14.6	73.0	967	18	US-10-425-115-77608
39	14.6	73.0	988	17	US-10-264-237-534
40	14.6	73.0	1125	18	US-10-439-247-19
41	14.6	73.0	1545	18	US-10-437-963-4248
42	14.6	73.0	2102	18	US-10-437-963-37126
43	14.6	73.0	3006	19	US-10-509-307-7
44	14.6	73.0	3459	18	US-10-437-963-70756
45	14.6	73.0	4299	19	US-10-887-553A-993
46	14.6	73.0	248436	13	US-10-087-192-2034
47	14.4	72.0	25	19	US-10-719-900-542459
48	14.4	72.0	300	18	US-10-437-963-59758
49	14.4	72.0	312	16	US-10-259-678-506
50	14.4	72.0	475	18	US-10-767-701-1959

ALIGNMENTS

RESULT 1
US-10-369-493-24476
Sequence 24476, Application US/10369493
Publication No. US20030233675A1
GENERAL INFORMATION:

APPLICANT: Cao, Yongwei
APPLICANT: Hinkle, Gregory J.
APPLICANT: Slater, Steven C.
APPLICANT: Goldman, Barry S.
APPLICANT: Chen, Xianfeng
TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF
FILE REFERENCE: 38-10(52052)B
CURRENT FILING DATE: 2003-02-28
PRIOR APPLICATION NUMBER: US 60/360,039
PRIOR FILING DATE: 2002-02-21
NUMBER OF SEQ ID NOS: 47374
SEQ ID NO 24476
LENGTH: 2547
TYPE: DNA
ORGANISM: Escherichia coli
US-10-369-493-24476

Query Match 86.0%; Score 17.2; DB 17; Length 2547;
Best Local Similarity 70.0%; Pred. No. 20;
Matches 14; Conservative 6; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGMGAYTAYTCACMGGYGC 20

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OM nucleic - nucleic search, using sw model

Run on: June 2, 2005, 07:12:26 ; Search time 134.492 Seconds

(without alignments)
5660.438 Million cell updates/sec

Title: US-10-088-117A-19

Perfect score: 20
Sequence: 1 gmgaytactbaccmggyc 20

Scoring table: IDENTITY NUC

Gapop 10.0, Gapext 1.0

Searched: 34239544 seqs, 19032134700 residues

Total number of hits satisfying chosen parameters: 68479088

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 50 summaries

Database :

EST:*

1: gb_est1:*
2: gb_est2:*
3: gb_hic:*
4: gb_est3:*
5: gb_est4:*
6: gb_est5:*
7: gb_est6:*
8: gb_gse1:*
9: gb_gse2:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
C 1	17.2	86.0	684	4	BG456299 NF076D03P
C 2	17.2	86.0	690	9	CL658599 PRI0131d
C 3	17.2	86.0	715	8	BH370263 AG-ND-105
C 4	17.2	86.0	716	6	CB088161 hm61b04.9
C 5	17.2	86.0	773	8	BH402590 AG-ND-137
C 6	17.2	86.0	794	9	CL669134 PRI0159c
C 7	17.2	86.0	799	8	BH388945 AG-ND-137
C 8	17.2	86.0	812	9	CL671059 PRI0163d
C 9	16.4	82.0	385	2	AW226349 ST81D01P
C 10	16	80.0	531	9	CW536619 OP_Ba003
C 11	16	80.0	795	9	CW531185 OP_Ba003
C 12	16	80.0	798	9	CW539148 OP_Ba005
C 13	16	80.0	846	2	BF182266 601804018
C 14	16	80.0	853	9	CW528614 OP_Ba004
C 15	16	80.0	902	9	CW505482 OP_Ba000
C 16	16	80.0	1088	9	AL419604 T7 end of
C 17	15.6	78.0	349	6	AU225724 AU225724
C 18	15.6	78.0	360	6	C48572 C48572 Yuji
C 19	15.6	78.0	360	6	C50548 C50548 Yuji
C 20	15.6	78.0	360	7	D75946 CELK112B6P
C 21	15.6	78.0	360	7	T00584 WEST01305 E
C 22	15.6	78.0	374	6	C48425 C48425 Yuji
C 23	15.6	78.0	376	1	AV194216 AV194216
C 24	15.6	78.0	378	1	AV194014 AV194014

25	15.6	78.0	389	6	C49840
26	15.6	78.0	401	1	AU207172
27	15.6	78.0	445	4	BJ119259
C 28	15.6	78.0	449	8	AO555032 RPCI-11-4
C 29	15.6	78.0	527	9	CC993846
30	15.6	78.0	531	4	BJ104489
31	15.6	78.0	531	6	CB402708
32	15.6	78.0	533	4	BJ109482
C 33	15.6	78.0	549	6	CB399218
34	15.6	78.0	555	7	CO112835
35	15.6	78.0	573	4	BJ104229
36	15.6	78.0	600	4	BJ112730
37	15.6	78.0	650	4	BJ762214
C 38	15.6	78.0	672	7	CN145218
C 39	15.6	78.0	703	9	CC788790
C 40	15.6	78.0	772	4	BI489224
41	15.6	78.0	787	8	BZ570305
C 42	15.6	78.0	790	9	CL241049
43	15.6	78.0	801	9	CC622684
C 44	15.6	78.0	804	7	CK775307
C 45	15.6	78.0	889	9	CG875316
46	15.6	78.0	974	9	CL433985
47	15.6	78.0	1030	9	AG332385
C 48	15.6	78.0	1057	9	CL263736
49	15.6	78.0	1095	4	BG298826
C 50	15.4	77.0	882	8	CC134127

ALIGNMENTS

RESULT 1
BG456299/c

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

684 bp mRNA linear EST 19-MAR-2001
NF076D03P1F1028 Phosphate starved leaf Medicago truncatula cDNA
clone NF076D03P1 5', mRNA sequence.

BG456299
BG456299.1 GI:13379624
EST.
Medicago truncatula (barrel medic)

Medicago truncatula
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; eurosids I; Fabales; Fabaceae; Papilionoideae; Trifolieae;
Medicago.

1 (bases 1 to 684)
Lin,J.,Scott,A.D., Harris,A.R., Gonzales,R.A., Bell,C.J.,
Flores,H.R., Inman,J.T., Wellner,J.W., May,G.D. and Harrison,M.J.
Expressed Sequence Tags from the Samuel Roberts Noble Foundation
Medicago truncatula phosphate-starved leaf library
Unpublished (2000)

Contact: Harrison MJ
Plant Biology Division
The Samuel Roberts Noble Foundation
2510 Sam Noble Parkway, Ardmore, OK 73402, USA
Tel: 580 221 7325
Fax: 580 221 7380

Email: mharrison@noble.org
Insert Length: 684 Std Error: 0.00
Plate: 076 row: D column: 03
Seq primer: TCACACGAGAAACGCTATGAC.

Seq primer: TCACACGAGAAACGCTATGAC.
Location/Qualifiers
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/mol_type="mRNA"
/db_xref="taxon:3880"
/clone="NF076D03P1"
/tissue_type="leaf"
/dev_stage="trifoliolate"
/clone_libs="Phosphate starved leaf"
/note="Vector: Lambda Zap; At the trifoliolate stage, M.
truncatula plants were transplanted to phosphate-free sand
and grown for a further 30 days. During this 30 day

FEATURES
source

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OM nucleic - nucleic search, using sw model

Run on: June 1, 2005, 23:14:35 ; Search time 157.531 Seconds
(without alignments)
6151.841 Million cell updates/sec

Title: US-10-088-117A-20
Perfect score: 20
Sequence: 1 twygarcgyaacgymtcga 20
Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 4708233 seqs, 24227607955 residues
Total number of hits satisfying chosen parameters: 9416466

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 50 summaries

Database : GenEmbl.*
1: gb_ba.*
2: gb_hgt.*
3: gb_in.*
4: gb_om.*
5: gb_ov.*
6: gb_pat.*
7: gb_ph.*
8: gb_pl.*
9: gb_pr.*
10: gb_ro.*
11: gb_sts.*
12: gb_sy.*
13: gb_un.*
14: gb_vl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	17.6	88.0	20	6	AX098623 Sequence
2	17.6	88.0	2292	1	RSU25037
3	17.6	88.0	2475	6	AX098610 Sequence
4	17.6	88.0	2486	6	AX098605 Sequence
5	17.6	88.0	2487	6	AX098604 Sequence
6	17.6	88.0	2487	6	AX098606 Sequence
7	17.6	88.0	2490	1	SPU5974
8	17.6	88.0	2523	6	AX098609 Sequence
9	17.6	88.0	2540	1	RCDSTNORG
10	17.6	88.0	2544	6	AX098612 Sequence
11	17.6	88.0	2750	1	RCADMSA
12	17.6	88.0	3316	1	RCADMS
13	17.6	88.0	4680	1	ECTOR
14	17.6	88.0	5637	1	RCU49506
15	17.6	88.0	6915	1	SWA6085
16	17.6	88.0	7990	1	AF016236
17	17.6	88.0	10726	1	AE015567
18	17.6	88.0	11289	1	AE005293
19	17.6	88.0	11378	1	AE002060

20	17.6	88.0	13067	1	AE015128
21	17.6	88.0	18252	1	D90737
22	17.6	88.0	19650	1	D90736
23	17.6	88.0	22418	1	AE008878
24	17.6	88.0	110000	1	U00096.10
25	17.6	88.0	214311	2	ACU10537
26	17.6	88.0	245050	1	AL627280
27	17.6	88.0	292504	1	AE016981
28	17.6	88.0	300350	1	AP006574
29	17.6	88.0	300592	1	AE016846
30	17.6	88.0	301276	1	AE016758
31	17.6	88.0	327773	1	AP002554
32	16.6	83.0	13013	1	AP008592
33	16.6	83.0	35909	3	LMFL3856
34	16.6	83.0	110000	1	AE000516.15
35	16.6	83.0	299450	1	EX248338
36	16.6	83.0	311281	1	AE016859
37	16.6	83.0	348264	1	EX842576
38	16.4	82.0	2501	8	AY260969
39	16	80.0	174	6	CO604041
40	16	80.0	825	6	AX413746
41	16	80.0	825	6	AX415759
42	16	80.0	1389	6	CO647060
43	16	80.0	1992	6	AX608309
44	16	80.0	2099	6	AX414956
45	16	80.0	2544	6	CO604040
46	16	80.0	3558	6	AX416768
47	16	80.0	4122	6	CO579074
48	16	80.0	5397	6	CO581777
49	16	80.0	10362	1	AE014922
50	16	80.0	10715	1	AE006216

ALIGNMENTS

RESULT 1	AX098623	Sequence 20 from Patent WO0120030.	20 bp	DNA	linear	PAT 02-APR-2001
LOCUS	AX098623	Sequence 20 from Patent WO0120030.				
DEFINITION	AX098623	Sequence 20 from Patent WO0120030.				
ACCESSION	AX098623.1	GI:13537884				
VERSION	AX098623.1	GI:13537884				
KEYWORDS		synthetic construct				
SOURCE		other sequences; artificial sequences.				
ORGANISM		Giordano, G., dos Santos, J.P. and Mejean, V.				
REFERENCE		Nucleotide sequences derived from genes coding for trimethylamine				
AUTHORS		n-oxide reductase, uses thereof in particular for detecting				
TITLE		bacteria				
JOURNAL		Patent: WO 0120030-A 20 22-MAR-2001;				
FEATURES		CENTRE NATIONAL DE LA RECHERCHE SCIENTIFIQUE (CNRS) (FR)				
source		Location/Qualifiers				
		1..20				
		/organism="synthetic construct"				
		/mol_type="unassigned DNA"				
		/db_xref="taxon:32630"				
		/note="amorce PCR"				
ORIGIN						
Query Match		88.0%; Score 17.6; DB 6; Length 20;				
Best Local Similarity		100.0%; Pred. No. 87;				
Matches		20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;				
QY	1	TWYGARCGYAACGAYMTCGA 20				
Db	1	TWYGARCGYAACGAYMTCGA 20				
RESULT 2						
RSU25037						
LOCUS						

linear BCT 16-APR-1998

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OM nucleic - nucleic search, using sw model

Run on: June 1, 2005, 22:48:55 ; Search time 19.9769 Seconds
(without alignments)
5926.580 Million cell updates/sec

Title: US-10-088-117A-20
Perfect score: 20
Sequence: 1 twygarcyaaacgaymtega 20

Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 4390206 seqs, 2959870667 residues

Total number of hits satisfying chosen parameters: 8780412

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 50 summaries

Database : N Geneseq_16Dec04:*

- 1: Geneseqn1980s:*
- 2: Geneseqn1990s:*
- 3: Geneseqn2000s:*
- 4: Geneseqn2001as:*
- 5: Geneseqn2001bs:*
- 6: Geneseqn2002as:*
- 7: Geneseqn2002bs:*
- 8: Geneseqn2003as:*
- 9: Geneseqn2003bs:*
- 10: Geneseqn2003cs:*
- 11: Geneseqn2003ds:*
- 12: Geneseqn2004as:*
- 13: Geneseqn2004bs:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	17.6	88.0	20	AAf79959	AAf79959 PCR prime
2	17.6	88.0	812	ABQ39018	ABQ39018 Oligonucleotide
3	17.6	88.0	812	ABQ39019	ABQ39019 Oligonucleotide
4	17.6	88.0	2475	AAf79948	AAf79948 Nucleotide
5	17.6	88.0	2486	AAf79944	AAf79944 Nucleotide
6	17.6	88.0	2487	AAf79945	AAf79945 Nucleotide
7	17.6	88.0	2487	AAf79943	AAf79943 Nucleotide
8	17.6	88.0	2523	AAf79947	AAf79947 Nucleotide
9	17.6	88.0	2544	AAf79949	AAf79949 Nucleotide
10	17.6	88.0	2547	AAf79946	AAf79946 Nucleotide
11	17.6	88.0	2853	AAf79908	AAf79908 DNA encod
12	17.6	88.0	2853	AAf79906	AAf79906 DNA encod
13	17.6	88.0	2853	AAf79927	AAf79927 DNA encod
14	17.6	88.0	2853	AAf79945	AAf79945 DNA encod
15	17.6	88.0	11275	AAf79947	AAf79947 E. coli g
16	16.6	83.0	4689	AAf79949	AAf79949 Bacterial
17	16.6	83.0	110000	AAf79949	AAf79949 DNA encod
18	16.6	83.0	110000	AAf79949	AAf79949 DNA encod
19	16.4	82.0	1520	AAf79949	AAf79949 DNA encod
20	16.4	82.0	1520	AAf79949	AAf79949 DNA encod

C 21	16	80.0	174	4	ABL23039	ABL23039 Drosophil
C 22	16	80.0	547	6	ABQ32142	ABQ32142 Oligonucleotide
C 23	16	80.0	547	6	ABQ32143	ABQ32143 Oligonucleotide
C 24	16	80.0	825	6	ABQ69937	ABQ69937 Listeria
C 25	16	80.0	825	6	ABQ69937	ABQ69937 Listeria
C 26	16	80.0	1080	4	AAH52069	AAH52069 Mycobacte
C 27	16	80.0	1989	6	AAH68052	AAH68052 Streptoco
C 28	16	80.0	2099	6	ABQ69134	ABQ69134 Listeria
C 29	16	80.0	2544	4	ABL23038	ABL23038 Drosophil
C 30	16	80.0	3558	6	ABQ70946	ABQ70946 Listeria
C 31	16	80.0	4122	4	ABL06394	ABL06394 Drosophil
C 32	16	80.0	5397	4	ABL08196	ABL08196 Drosophil
C 33	16	80.0	110000	4	AAI99682_36	Continuation (37 o
C 34	16	80.0	110000	4	AAI99683_36	Continuation (37 o
C 35	16	80.0	110000	6	ABN71527_14	Continuation (15 o
C 36	16	80.0	110000	6	ABA03041_10	Continuation (11 o
C 37	15.6	78.0	471	11	ABD17626	ABD17626 Pseudomon
C 38	15.6	78.0	544	6	ABQ17749	ABQ17749 Oligonucleotide
C 39	15.6	78.0	544	6	ABQ17748	ABQ17748 Oligonucleotide
C 40	15.6	78.0	963	11	ABD17764	ABD17764 Pseudomon
C 41	15.6	78.0	1557	11	ABD17520	ABD17520 Pseudomon
C 42	15.6	78.0	1563	11	ABD17874	ABD17874 Pseudomon
C 43	15.6	78.0	2328	13	ADT45718	ADT45718 Bacterial
C 44	15.4	77.0	25	4	AAf79953	AAf79953 PCR prime
C 45	15.4	77.0	327	6	ABN18330	ABN18330 Human ORF
C 46	15.4	77.0	1008	8	ACA26292	ACA26292 Prokaryot
C 47	15.4	77.0	1128	10	ADC52112	ADC52112 DNA encod
C 48	15.4	77.0	1202	4	ABL53352	ABL53352 Mushroo
C 49	15.4	77.0	1202	5	ABL53444	ABL53444 Glycero
C 50	15.4	77.0	2084	4	ABL26475	ABL26475 Drosophil

ALIGNMENTS

RESULT 1

AAf79959
ID AAF79959 standard; DNA; 20 BP.

AC AAF79959;

DT 11-JUN-2001 (first entry)

DE PCR primer used to amplify trimethylamine N-oxide reductase genes.

KW torA gene; trimethylamine N-oxide reductase; flesh degradation;

KW spoilage bacteria; fish; crustacean; PCR primer; ss.

OS Synthetic.

PN WO200120030-A2.

PD 22-MAR-2001.

XX 15-SEP-2000; 2000WO-FR002578.

XX 15-SEP-1999; 99FR-00011543.

XX (CNRS) CENT NAT RECH SCI.

PI Giordano G, Dos Santos J, Mejean V;

DR WPI; 2001-244822/25.

XX Detecting bacteria that cause flesh degradation in fish, for testing
PT freshness, comprises using probes or primers based on the trimethylamine
PT N-oxide reductase system.

PS Claim 7; Page 42; 91pp; French.

XX PCR primers AAF79951-66 represent PCR primers used to amplify torA and
CC torC genes. TorA and torC are bacterial proteins of the trimethylamine N-
CC oxide reductase system. TorA nucleic acids are used for detecting, in a

Result No.	Query			DB	ID	Description
	Score	Match	Length			
C 1	16.6	83.0	4403765	3	US-09-103-840A-2	Sequence 2, Appl
C 2	16.6	83.0	4411529	3	US-09-103-840A-1	Sequence 1, Appl
C 3	15.6	78.0	471	4	US-09-252-991A-16230	Sequence 16230, A
C 4	15.6	78.0	963	4	US-09-252-991A-16368	Sequence 16368, A
C 5	15.6	78.0	1557	4	US-09-252-991A-16124	Sequence 16124, A
C 6	15.6	78.0	1563	4	US-09-252-991A-16478	Sequence 16478, A
C 7	15.4	77.0	491	4	US-09-270-767-1118	Sequence 1118, Ap
C 8	15.4	77.0	491	4	US-09-270-767-16400	Sequence 16400, A
C 9	15	75.0	622	4	US-09-270-767-25891	Sequence 25891, A
C 10	15	75.0	627	4	US-09-252-991A-5388	Sequence 5388, Ap
C 11	15	75.0	639	4	US-09-252-991A-5385	Sequence 5385, Ap
C 12	15	75.0	891	4	US-09-252-991A-5380	Sequence 5380, Ap
C 13	15	75.0	1095	4	US-09-489-039A-5797	Sequence 5797, Ap
C 14	15	75.0	1191	4	US-09-252-991A-5587	Sequence 5587, Ap
C 15	15	75.0	1206	4	US-09-252-991A-5642	Sequence 5642, Ap
C 16	15	75.0	1266	4	US-09-252-991A-5552	Sequence 5552, Ap
C 17	15	75.0	1292	4	US-09-270-767-11046	Sequence 11046, A
C 18	15	75.0	1356	4	US-09-270-767-10484	Sequence 10484, A
C 19	15	75.0	1494	4	US-09-710-279-2811	Sequence 2811, Ap
C 20	15	75.0	2277	3	US-09-134-001C-1751	Sequence 1751, Ap
C 21	15	75.0	3219	4	US-09-710-279-3691	Sequence 3691, Ap
C 22	15	75.0	3305	4	US-09-710-279-3844	Sequence 3844, Ap
C 23	15	75.0	3312	4	US-09-710-279-4308	Sequence 4308, Ap
C 24	15	75.0	9217	4	US-09-634-238-402	Sequence 402, App
C 25	15	75.0	4403765	3	US-09-103-840A-2	Sequence 2, Appl
C 26	15	75.0	4411529	3	US-09-103-840A-1	Sequence 1, Appl
C 27	14.8	74.0	428	4	US-09-270-767-10072	Sequence 10072, A

Result No.	Score	Query Match	Length	DB	ID	Description
C 1	17.6	88.0	812	18	US-10-363-345A-25609	Sequence 25609, A
C 2	17.6	88.0	812	18	US-10-363-345A-25610	Sequence 25610, A
C 3	17.6	88.0	812	19	US-10-363-483A-25609	Sequence 25609, A
C 4	17.6	88.0	812	19	US-10-363-483A-25610	Sequence 25610, A
C 5	17.6	88.0	2547	17	US-10-369-493-24476	Sequence 24476, A
C 6	17.6	88.0	12175	16	US-10-240-689-39	Sequence 39, A
C 7	16.6	83.0	4689	17	US-10-282-122A-33564	Sequence 33564, A
C 8	16.4	82.0	204	18	US-10-425-115-8983	Sequence 8983, Ap
C 9	16.4	82.0	1520	18	US-10-363-345A-30991	Sequence 30991, A
C 10	16.4	82.0	1520	18	US-10-363-345A-30992	Sequence 30992, A
C 11	16.4	82.0	1520	19	US-10-363-483A-30991	Sequence 30991, A
C 12	16.4	82.0	1520	19	US-10-363-483A-30992	Sequence 30992, A

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OM nucleic - nucleic search, using sw model

Run on: June 2, 2005, 07:12:26 ; Search time 134.492 Seconds
(without alignments)
5660.438 Million cell updates/sec

Title: US-10-088-117a-20
Perfect score: 20
Sequence: 1 twygarcgyaacgymtcga 20
Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 34239544 seqs, 190321134700 residues
Total number of hits satisfying chosen parameters: 68479088

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 50 summaries

Database : EST.*
1: gb_est1:*
2: gb_est2:*
3: gb_hic:*
4: gb_est3:*
5: gb_est4:*
6: gb_est5:*
7: gb_est6:*
8: gb_gss1:*
9: gb_gss2:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	17.6	88.0	636	4	BG859034
2	17.6	88.0	687	5	BQ157381
3	16.6	83.0	522	7	CF843239
4	16.6	83.0	608	7	CF843217
5	16.6	83.0	712	7	CF841741
6	16.4	82.0	673	7	CF638575
7	16.4	82.0	736	7	CO147437
8	16	80.0	353	4	BG955182
9	16	80.0	382	9	CL879226
10	16	80.0	430	6	CD061642
11	16	80.0	431	6	CD061662
12	16	80.0	443	6	CD061564
13	16	80.0	443	7	CO320509
14	16	80.0	474	6	CD870126
15	16	80.0	493	5	BP092642
16	16	80.0	510	4	BG653512
17	16	80.0	514	9	TAL14G02Q
18	16	80.0	534	7	CF760096
19	16	80.0	548	4	BI624576
20	16	80.0	555	4	BI510862
21	16	80.0	594	8	BH766340
22	16	80.0	604	6	CA065149
23	16	80.0	612	8	BH768548
24	16	80.0	646	6	CA083457

25	16	80.0	684	8	BH002877
c 26	16	80.0	688	7	CO203373
c 27	16	80.0	725	5	BW014949
28	16	80.0	776	7	CO983335
29	16	80.0	803	4	BI825116
c 30	16	80.0	810	9	CG067730
31	16	80.0	896	4	BF978318
32	16	80.0	970	9	AG118710
33	16	80.0	1118	7	CK208312
34	15.6	78.0	347	5	BX548735
35	15.6	78.0	367	8	AZ142355
36	15.6	78.0	526	4	BU650234
c 37	15.6	78.0	530	1	AV714335
c 38	15.6	78.0	624	8	BH463715
39	15.6	78.0	653	9	CR3339872
40	15.6	78.0	762	8	BZ570281
41	15.6	78.0	824	2	BF248110
c 42	15.6	78.0	830	9	CG893568
c 43	15.6	78.0	892	2	BF028251
c 44	15.6	78.0	1015	8	BH656450
c 45	15.4	77.0	242	6	CB040958
c 46	15.4	77.0	400	5	BP665167
c 47	15.4	77.0	448	5	BP583126
c 48	15.4	77.0	499	7	CO278219
c 49	15.4	77.0	520	7	CO321105
c 50	15.4	77.0	555	5	BW029423

ALIGNMENTS

RESULT 1
BG859034
LOCUS
DEFINITION
1024061A05.y1 C. reinhardtii CC-1690, normalized, Lambda Zap II
ACCESSION
BG859034
VERSION
BG859034.1 GI:14240218
KEYWORDS
EST.
SOURCE
Chlamydomonas reinhardtii
ORGANISM
Chlamydomonas reinhardtii
Eukaryota; Viridiplantae; Chlorophyta; Chlorophyceae; Volvocales;
Chlamydomonadales; Chlamydomonas.
REFERENCE
1 (bases 1 to 636)
AUTHORS
Grossman, A., Davies, J., Federspiel, N., Harris, E., Lefebvre, P.,
McDermott, J.P., Silflow, C., Stern, D. and Surzycki, R.
TITLE
Analyses of the Chlamydomonas reinhardtii Genome: A Model,
Unicellular System for Analyzing Gene Function and Regulation in
Vascular Plants; project phase 2
JOURNAL
Unpublished (2000)
COMMENT
Contact: Charles Hauser
DCMB Box 91000
Duke University
Durham, NC 27708-1000
Tel: 919 613 8159
Fax: 919 613 8177
Email: chauser@duke.edu.
FEATURES
source
1..636
Location/Qualifiers
/organism="Chlamydomonas reinhardtii"
/mol_type="mRNA"
/strain="CC-1690 wild type mt+ 21gr"
/db_xref="taxon:3055"
/clone_lib="C. reinhardtii CC-1690, normalized, Lambda Zap
II"
/note="Vector: pBluescript II SK-; Site 1: EcoRI; Site 2:
XhoI; This library, constructed by John Davies and Jeffrey
McDermott, combines cDNAs from CC-1690 cells grown to
mid-log phase in TAP (acetate-containing) medium in the
light, TAP medium in the dark, HS (minimal) medium in
ambient levels of CO2 and HS medium bubbled with 5% CO2.
PolyA mRNA was purified from each sample, pooled and cDNA
synthesized. The cDNA was directionally cloned into lambda

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OM nucleic - nucleic search, using sw model

Run on: June 1, 2005, 23:14:35 ; Search time 157.531 Seconds
(without alignments)
6151.841 Million cell updates/sec

Title: US-10-088-117A-21

Perfect score: 20

Sequence: 1 ggyvrtaccabscvcttc 20

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 4708233 seqs, 24227607955 residues

Total number of hits satisfying chosen parameters: 9416466

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 50 summaries

Database :

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3: gb_in.*
4: gb_om.*
5: gb_ov.*
6: gb_pat.*
7: gb_ph.*
8: gb_pl.*
9: gb_pr.*
10: gb_ro.*
11: gb_sts.*
12: gb_sy.*
13: gb_un.*
14: gb_vl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	16.4	82.0	20	6	AX098624
2	16.4	82.0	100	6	AX989852
3	16.4	82.0	100	6	AX997781
4	16.4	82.0	2075	6	AX098610
5	16.4	82.0	2486	6	AX098605
6	16.4	82.0	2487	6	AX098604
7	16.4	82.0	2487	6	AX098606
8	16.4	82.0	2490	1	SPU5974
9	16.4	82.0	2540	1	RCDS1NORG
10	16.4	82.0	2544	6	AX098612
11	16.4	82.0	3211	1	ECOCBPA
12	16.4	82.0	4680	1	ECTOR
13	16.4	82.0	5637	1	RC049506
14	16.4	82.0	6492	1	ECODMS
15	16.4	82.0	6915	1	SMA6085
16	16.4	82.0	9994	1	AE001526
17	16.4	82.0	10726	1	AE015567
18	16.4	82.0	11860	1	U32747
19	16.4	82.0	12302	1	AE005279

c 20	16.4	82.0	12582	1	AE015114	Shigella
c 21	16.4	82.0	13067	1	AE015128	Shigella
c 22	16.4	82.0	16210	1	D90727	Escherichia
c 23	16.4	82.0	18252	1	D90737	Escherichia
c 24	16.4	82.0	19650	1	D90736	Escherichia
c 25	16.4	82.0	22418	1	AE008878	Salmonell
c 26	16.4	82.0	25409	1	AE008741	Salmonell
c 27	16.4	82.0	110000	1	U00096_09	Continuation (10 o
c 28	16.4	82.0	110000	1	U00096_10	Continuation (11 o
c 29	16.4	82.0	110000	6	BD426631_06	Continuation (7 of
c 30	16.4	82.0	110000	6	AR274513_06	Continuation (7 of
c 31	16.4	82.0	110000	6	AR541453_06	Continuation (7 of
c 32	16.4	82.0	245050	1	AL627280	Salmonell
c 33	16.4	82.0	250950	1	AP005335	Vibrio vu
c 34	16.4	82.0	292504	1	AE016981	Shigella
c 35	16.4	82.0	294050	1	AL627268	Salmonell
c 36	16.4	82.0	297816	1	AP002553	Escherich
c 37	16.4	82.0	299130	1	AP005077	Vibrio pa
c 38	16.4	82.0	300592	1	AE016846	Salmonell
c 39	16.4	82.0	301276	1	AE016758	Escherich
c 40	16.4	82.0	301983	1	AE016840	Salmonell
c 41	16.4	82.0	304490	1	AE016806	Vibrio vu
c 42	16.4	82.0	349080	1	CR378667	Photobact
c 43	15.6	78.0	110000	1	AE016827_05	Continuation (6 of
c 44	15.6	78.0	300540	1	AE017154	Haemophil
c 45	15.6	78.0	314150	1	CJ11168X1	Campyloba
c 46	15.6	78.0	348672	1	CR378670	Photobact
c 47	15.4	77.0	1641	6	BD269438	Mitomycin
c 48	15.4	77.0	1641	6	AR266924	Sequence
c 49	15.4	77.0	10447	1	AE000556	Helicobac
c 50	15.4	77.0	53500	6	BD269447	Mitomycin

ALIGNMENTS

RESULT 1	AX098624	AX098624	20 bp	DNA	linear	PAT 02-APR-2001
LOCUS	Sequence 21 from Patent WO0120030.					
DEFINITION	AX098624					
ACCESSION	AX098624.1	GI:13537885				
VERSION						
KEYWORDS	synthetic construct					
SOURCE	synthetic construct					
ORGANISM	other sequences; artificial sequences.					
REFERENCE	1					
AUTHORS	Giordano, G., dos Santos, J.P. and Mejean, V.					
TITLE	Nucleotide sequences derived from genes coding for trimethylamine n-oxide reductase, uses thereof in particular for detecting bacteria					
JOURNAL	Patent: WO 0120030-A 21 22-MAR-2001;					
FEATURES	CENTRE NATIONAL DE LA RECHERCHE SCIENTIFIQUE (CNRS) (FR)					
source	Location/Qualifiers					
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	/organism="synthetic construct"					
	/mol_type="unassigned DNA"					
	/db_xref="taxon:32630"					
	/note="amorce PCR"					
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Query Match	82.0%; Score 16.4; DB 6; Length 20;					
Best Local Similarity	100.0%; Pred.No. 3.1e+02;					
Matches	20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;					
Qy	1 GGVYCTACCAACVCCCTTC 20					
Db	1 GGVYCTACCAACVCCCTTC 20					
RESULT 2						
AX989852/c						
LOCUS	AX989852	100 bp	DNA	linear	PAT 16-JAN-2004	

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OM nucleic - nucleic search, using sw model
Run on: June 1, 2005, 22:48:55 ; Search time 19.9769 seconds
(without alignments)
5926.580 Million cell updates/sec

Title: US-10-088-117A-21
Perfect score: 20
Sequence: 1 ggyvrtaccabscvcttc 20

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 4390206 seqs, 2959870667 residues

Total number of hits satisfying chosen parameters: 8780412

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 50 summaries

Database : N_Geneseq_16Dec04:*
1: Geneseqn1980s:*
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4: Geneseqn2001as:*
5: Geneseqn2001bs:*
6: Geneseqn2002as:*
7: Geneseqn2002bs:*
8: Geneseqn2003as:*
9: Geneseqn2003bs:*
10: Geneseqn2003ds:*
11: Geneseqn2003ds:*
12: Geneseqn2004as:*
13: Geneseqn2004bs:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	16.4	82.0	20	Aaf79960	Aaf79960 PCR prime
2	16.4	82.0	100	ACD77968	AcD77968 E. coli K
3	16.4	82.0	100	ACD70045	AcD70045 E. coli K
4	16.4	82.0	1338	Aas88390	Aas88390 DNA encod
5	16.4	82.0	1887	Aah19221	Aah19221 Human sec
6	16.4	82.0	2358	ACA19185	ACA19185 Prokaryot
7	16.4	82.0	2358	ADS46037	ADS46037 Bacterial
8	16.4	82.0	2413	ACA49353	ACA49353 Prokaryot
9	16.4	82.0	2445	ACA51180	ACA51180 Prokaryot
10	16.4	82.0	2445	ACA51914	ACA51914 Prokaryot
11	16.4	82.0	2475	Aaf79948	Aaf79948 Nucleotid
12	16.4	82.0	2486	Aaf79944	Aaf79944 Nucleotid
13	16.4	82.0	2487	Aaf79945	Aaf79945 Nucleotid
14	16.4	82.0	2487	Aaf79943	Aaf79943 Nucleotid
15	16.4	82.0	2544	Aaf79949	Aaf79949 Nucleotid
16	16.4	82.0	2547	ADS46046	ADS46046 Bacterial
17	16.4	82.0	3712	Aah19184	Aah19184 Human sec
18	16.4	82.0	11275	Aah43717	Aah43717 E. coli g
19	16.4	82.0	110000	2 AAF79943	Continuation (7 of
20	15.4	77.0	1641	3 AAC55833	AAC55833 S. lavend

21	15.4	77.0	1641	10	ADe10252	Adel0252 S. lavend
22	15.4	77.0	53500	3	AAC55842	Aac55842 Complete
23	15.4	77.0	53500	10	ADe10261	Adel0261 S. lavend
c	24	14.8	74.0	129	5	ABX15064 Human ner
25	14.8	74.0	395	8	ABX45119	Abx45119 Bovine ES
26	14.8	74.0	442	8	ABX46058	Abx46058 Bovine ES
27	14.8	74.0	519	8	ABZ53408	Abz53408 Aspergill
c	28	14.8	74.0	804	5	AAS85095 DNA encod
29	14.8	74.0	1176	5	AAS65036	Aas65036 DNA encod
c	30	14.8	74.0	1597	13	ADs48720 Bacterial
31	14.8	74.0	1794	3	AAa30256	Aaa30256 Rat parti
c	32	14.8	74.0	1913	13	ACn37272 Tumour-as
c	33	14.8	74.0	2268	8	ACA31543 Prokaryot
34	14.8	74.0	2280	13	ABD33563	Abd33563 Human can
35	14.8	74.0	2286	12	ADi81563	Adi81563 Rat stre
36	14.8	74.0	2286	12	ADi81575	Adi81575 Rat vanil
37	14.8	74.0	2289	12	ADi81627	Adi81627 Rat ion c
c	38	14.8	74.0	2310	6	AAS94752 Human DNA
c	39	14.8	74.0	2319	6	ABZ82575 Human sec
c	40	14.8	74.0	2436	8	ACA35519 Prokaryot
c	41	14.8	74.0	2478	11	ACH99175 Klebsiell
c	42	14.8	74.0	2523	4	AAF79947 Nucleotid
c	43	14.8	74.0	2597	6	ABK70006 cDNA enco
c	44	14.8	74.0	2597	9	ADA01359 Human PRO
c	45	14.8	74.0	2597	9	ADA43788 Human CDN
c	46	14.8	74.0	2597	9	ADA43556 Human CDN
c	47	14.8	74.0	2597	9	ADA01231 Human PRO
c	48	14.8	74.0	2597	9	ADA01115 Human CDN
c	49	14.8	74.0	2597	9	ADA43672 Human CDN
c	50	14.8	74.0	2597	9	ADA06934 Human PRO

ALIGNMENTS

RESULT 1
AAF79960
ID AAF79960 standard; DNA; 20 BP.

AC AAF79960;
DT 11-JUN-2001 (first entry)

DE PCR primer used to amplify trimethylamine N-oxide reductase genes.

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: June 2, 2005, 08:20:11 ; Search time 6.17692 Seconds
(without alignments)
5298.032 Million cell updates/sec

Title: US-10-088-117A-21

Perfect score: 20

Sequence: 1 ggyvrtaccabscvcccttc 20

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 1202784 seqs, 818138359 residues

Total number of hits satisfying chosen parameters: 2405568

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 50 summaries

Database : Issued Patents NA:*

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3: /cgm2_6/ptodata/1/ina/6A COMB.seq:*

4: /cgm2_6/ptodata/1/ina/6B COMB.seq:*

5: /cgm2_6/ptodata/1/ina/PTCUS COMB.seq:*

6: /cgm2_6/ptodata/1/ina/backfiles1.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	16.4	82.0	1830121	4	US-09-557-884-1
2	16.4	82.0	1830121	4	US-09-643-990A-1
3	15.4	77.0	1641	4	US-09-266-965-67
4	15.4	77.0	53500	4	US-09-266-965-76
5	14.8	74.0	2478	4	US-09-489-039A-4970
6	14.8	74.0	2736	3	US-09-235-451-3
7	14.8	74.0	2736	4	US-09-978-303-3
8	14.4	72.0	654	4	US-09-891-641-72
9	14.4	72.0	1305	4	US-09-902-540-6383
10	14.4	72.0	2492	4	US-09-902-540-421
11	14.4	72.0	128516	4	US-09-949-016-13501
12	14.4	72.0	133157	4	US-09-949-016-12541
13	14.2	71.0	3343	4	US-09-503-890-1
14	14.0	70.0	307	4	US-09-621-976-11201
15	14.0	70.0	601	4	US-09-949-016-67294
16	14.0	70.0	2451	4	US-09-543-681A-427
17	14.0	70.0	3425	4	US-09-800-971-1
18	14.0	70.0	13953	3	US-09-738-884-3
19	14.0	70.0	13953	4	US-10-096-961A-3
20	14.0	70.0	36307	4	US-09-949-016-17372
21	14.0	70.0	100463	4	US-09-949-016-12511
22	14.0	70.0	100468	4	US-09-949-016-13725
23	14.0	70.0	189560	4	US-09-949-016-17202
24	13.8	69.0	219	4	US-09-489-039A-7065
25	13.8	69.0	601	4	US-09-949-016-135221
26	13.8	69.0	601	4	US-09-949-016-170678
27	13.8	69.0	647	4	US-09-777-430C-72

28	13.8	69.0	661	4	US-09-814-915A-104	Sequence 104, App
29	13.8	69.0	725	4	US-09-591-992-3	Sequence 3, Appli
30	13.8	69.0	725	4	US-09-023-655-1344	Sequence 1344, Ap
31	13.8	69.0	741	3	US-07-927-391-25	Sequence 25, Appl
32	13.8	69.0	741	4	US-09-023-655-1165	Sequence 1165, Ap
33	13.8	69.0	752	6	5212073-1	Patent No. 5212073
34	13.8	69.0	752	6	5212073-1	Patent No. 5212073
35	13.8	69.0	772	4	US-08-437-306-1	Sequence 1, Appli
36	13.8	69.0	849	4	US-09-902-540-6085	Sequence 6085, Ap
37	13.8	69.0	1555	4	US-09-902-540-267	Sequence 267, App
38	13.8	69.0	1712	4	US-09-148-545-106	Sequence 106, App
39	13.8	69.0	1822	4	US-09-148-545-105	Sequence 105, App
40	13.8	69.0	2417	4	US-09-216-393B-306	Sequence 306, App
41	13.8	69.0	2417	4	US-09-216-393B-308	Sequence 308, App
42	13.8	69.0	6060	4	US-08-956-171E-534	Sequence 534, App
43	13.8	69.0	6060	4	US-08-781-98A-534	Sequence 534, App
44	13.8	69.0	10903	4	US-09-949-016-15530	Sequence 15530, A
45	13.8	69.0	15575	4	US-09-949-016-12634	Sequence 12634, A
46	13.8	69.0	15575	4	US-09-949-016-16568	Sequence 16568, A
47	13.8	69.0	33529	3	US-09-144-085-3	Sequence 3, Appli
48	13.8	69.0	42376	4	US-09-949-016-16276	Sequence 16276, A
49	13.8	69.0	48974	3	US-08-920-422-17	Sequence 17, Appl
50	13.8	69.0	50797	4	US-09-949-016-16346	Sequence 16346, A

ALIGNMENTS

RESULT 1

US-09-557-884-1

; Sequence 1, Application US/09557884

; Patent No. 6506581

; GENERAL INFORMATION:

; APPLICANT: Fleischmann et al.

; TITLE OF INVENTION: The Nucleotide sequence of

; the Haemophilus influenzae Rd Genome, Fragments

; Thereof, and Uses Thereof

; NUMBER OF SEQUENCES: 1

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Human Genome Sciences, Inc.

; STREET: 9410 Key West Avenue

; CITY: Rockville

; STATE: MD

; COUNTRY: USA

; ZIP: 20850

; COMPUTER READABLE FORM:

; MEDIUM TYPE: 3 1/2 inch diskette

; COMPUTER: Dell Pentium

; OPERATING SYSTEM: MS DOS v6.22

; SOFTWARE: ASCII Text

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/09/557,884

; FILING DATE: 25-Apr-2000

; CLASSIFICATION: <Unknown>

; PRIORITY APPLICATION DATA:

; APPLICATION NUMBER: 08/476,102

; FILING DATE: JUN-5-1995

; ATTORNEY/AGENT INFORMATION:

; NAME: Michelle S. Marks

; REGISTRATION NUMBER: 41,971

; REFERENCE/DOCKET NUMBER: P8186P3

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 301-309-8504

; TELEFAX: 301-309-8439

; INFORMATION FOR SEQ ID NO: 1:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 1830121 base pairs

; TYPE: nucleic acid

; STRANDEDNESS: double

; TOPOLOGY: linear

; SEQUENCE DESCRIPTION: SEQ ID NO: 1:

US-09-557-884-1

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OM nucleic - nucleic search, using sw model

Run on: June 2, 2005, 16:25:53 ; Search time 21.2846 Seconds
(without alignments)
5776.400 Million cell updates/sec

Title: US-10-088-117a-21

Perfect score: 20

Sequence: 1 ggyvrtaccabscvcttc 20

Scoring table: IDENTITY_NUC

Gapop 10.0, Gapext 1.0

Searched: 5706582 seqs, 3073711274 residues

Total number of hits satisfying chosen parameters: 11413164

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Listing first 50 summaries

Database : Published Applications NA:**

- 1: /cgn2_6/ptodata/2/pubpna/US07_PUBCOMB.seq.*
- 2: /cgn2_6/ptodata/2/pubpna/PCT_NEW_PUB.seq.*
- 3: /cgn2_6/ptodata/2/pubpna/US05_NEW_PUB.seq.*
- 4: /cgn2_6/ptodata/2/pubpna/US06_PUBCOMB.seq.*
- 5: /cgn2_6/ptodata/2/pubpna/US07_NEW_PUB.seq.*
- 6: /cgn2_6/ptodata/2/pubpna/PCTUS_PUBCOMB.seq.*
- 7: /cgn2_6/ptodata/2/pubpna/US08_NEW_PUB.seq.*
- 8: /cgn2_6/ptodata/2/pubpna/US08_PUBCOMB.seq.*
- 9: /cgn2_6/ptodata/2/pubpna/US09A_PUBCOMB.seq.*
- 10: /cgn2_6/ptodata/2/pubpna/US09B_PUBCOMB.seq.*
- 11: /cgn2_6/ptodata/2/pubpna/US09C_PUBCOMB.seq.*
- 12: /cgn2_6/ptodata/2/pubpna/US09_NEW_PUB.seq.*
- 13: /cgn2_6/ptodata/2/pubpna/US10A_PUBCOMB.seq.*
- 14: /cgn2_6/ptodata/2/pubpna/US10B_PUBCOMB.seq.*
- 15: /cgn2_6/ptodata/2/pubpna/US10C_PUBCOMB.seq.*
- 16: /cgn2_6/ptodata/2/pubpna/US10D_PUBCOMB.seq.*
- 17: /cgn2_6/ptodata/2/pubpna/US10E_PUBCOMB.seq.*
- 18: /cgn2_6/ptodata/2/pubpna/US10F_PUBCOMB.seq.*
- 19: /cgn2_6/ptodata/2/pubpna/US10_NEW_PUB.seq.*
- 20: /cgn2_6/ptodata/2/pubpna/US11_NEW_PUB.seq.*
- 21: /cgn2_6/ptodata/2/pubpna/US60_NEW_PUB.seq.*
- 22: /cgn2_6/ptodata/2/pubpna/US60_PUBCOMB.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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C 1	16.4	82.0	264	17	US-10-335-977-1903 Sequence 1903, Ap
C 2	16.4	82.0	348	17	US-10-335-977-1904 Sequence 1904, Ap
C 3	16.4	82.0	2358	17	US-10-369-493-24467 Sequence 24467, A
C 4	16.4	82.0	2358	17	US-10-282-122A-7055 Sequence 7055, Ap
C 5	16.4	82.0	2413	17	US-10-282-122A-37223 Sequence 37223, A
C 6	16.4	82.0	2445	17	US-10-282-122A-39050 Sequence 39050, A
C 7	16.4	82.0	2445	17	US-10-282-122A-39784 Sequence 39784, A
C 8	16.4	82.0	2547	17	US-10-369-493-24476 Sequence 24476, A
C 9	16.4	82.0	11275	16	US-10-240-689-39 Sequence 39, Appl
C 10	16.4	82.0	1830121	17	US-10-329-670-1 Sequence 1, Appli
C 11	16.4	82.0	1830121	18	US-10-158-865-1 Sequence 1, Appli

12	15.4	77.0	1641	10	US-09-953-348-67	Sequence 67, Appl
13	15.4	77.0	1641	15	US-10-267-255-67	Sequence 76, Appl
14	15.4	77.0	53500	10	US-09-953-348-76	Sequence 76, Appl
15	15.4	77.0	53500	15	US-10-267-255-76	Sequence 76, Appl
C 16	14.8	74.0	201	18	US-10-741-601-14846	Sequence 14846, A
C 17	14.8	74.0	201	19	US-10-741-600-37881	Sequence 37881, A
C 18	14.8	74.0	376	18	US-10-425-115-45319	Sequence 45319, A
19	14.8	74.0	395	9	US-09-960-352-10284	Sequence 10284, A
20	14.8	74.0	442	9	US-09-960-352-11223	Sequence 11223, A
21	14.8	74.0	517	13	US-10-027-632-129865	Sequence 129865, A
22	14.8	74.0	517	17	US-10-027-632-129865	Sequence 129865, A
C 23	14.8	74.0	656	17	US-10-424-599-26875	Sequence 26875, A
C 24	14.8	74.0	719	13	US-10-027-632-26627	Sequence 26627, A
C 25	14.8	74.0	719	17	US-10-027-632-26627	Sequence 26627, A
26	14.8	74.0	769	13	US-10-027-632-15109	Sequence 15109, A
27	14.8	74.0	769	17	US-10-027-632-15109	Sequence 15109, A
28	14.8	74.0	804	18	US-10-437-963-94508	Sequence 94508, A
C 29	14.8	74.0	1541	17	US-10-425-114-15108	Sequence 15108, A
C 30	14.8	74.0	1597	17	US-10-369-493-27150	Sequence 27150, A
C 31	14.8	74.0	1615	17	US-10-424-599-26876	Sequence 26876, A
C 32	14.8	74.0	1937	19	US-10-887-553A-387	Sequence 387, App
C 33	14.8	74.0	2268	17	US-10-282-122A-19413	Sequence 19413, A
34	14.8	74.0	2280	18	US-10-322-281-765	Sequence 765, App
35	14.8	74.0	2286	17	US-10-342-844-33	Sequence 33, Appl
36	14.8	74.0	2286	17	US-10-342-844-45	Sequence 45, Appl
37	14.8	74.0	2289	17	US-10-342-844-97	Sequence 97, Appl
C 38	14.8	74.0	2310	16	US-10-240-965-7	Sequence 7, Appli
C 39	14.8	74.0	2436	17	US-10-282-122A-23389	Sequence 23389, A
C 40	14.8	74.0	2597	14	US-10-245-752-91	Sequence 91, Appl
C 41	14.8	74.0	2597	14	US-10-245-859-91	Sequence 91, Appl
C 42	14.8	74.0	2597	14	US-10-245-103-91	Sequence 91, Appl
C 43	14.8	74.0	2597	14	US-10-245-107-91	Sequence 91, Appl
C 44	14.8	74.0	2597	14	US-10-245-143-91	Sequence 91, Appl
C 45	14.8	74.0	2597	14	US-10-245-771-91	Sequence 91, Appl
C 46	14.8	74.0	2597	14	US-10-245-851-91	Sequence 91, Appl
C 47	14.8	74.0	2597	14	US-10-245-883-91	Sequence 91, Appl
C 48	14.8	74.0	2597	14	US-10-237-535-91	Sequence 91, Appl
C 49	14.8	74.0	2597	14	US-10-238-183-91	Sequence 91, Appl
C 50	14.8	74.0	2597	14	US-10-238-283-91	Sequence 91, Appl

ALIGNMENTS

RESULT 1
US-10-335-977-1903/c
; Sequence 1903, Application US/10335977
; Publication No. US20040052799A1
; GENERAL INFORMATION:
; APPLICANT: DOUGLAS SMITH et al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES
; RELATING TO HELICOBACTER PYLORI FOR
; DIAGNOSTICS AND THERAPEUTICS
; NUMBER OF SEQUENCES: 10031
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: LAHIVE & COCKFIELD
; STREET: 28 State Street
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02109-1875
; COMPUTER READABLE FORM:
; MEDIUM TYPE: CD-ROM ISO9660
; COMPUTER: IBM PC Compatible
; OPERATING SYSTEM: Windows NT 4.0
; SOFTWARE: UNIX
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/335.977
; FILING DATE: 30-Dec-2002
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/993,002
; FILING DATE: 17-DEC-1997
; ATTORNEY/AGENT INFORMATION:

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OM nucleic - nucleic search, using sw model

Run on: June 2, 2005, 07:12:26 ; Search time 134.492 Seconds
(without alignments)
5660.438 Million cell updates/sec

Title: US-10-088-117A-21

Perfect score: 20

Sequence: 1 ggyvccrtaccabscvcttc 20

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 34239544 seqs, 19032134700 residues

Total number of hits satisfying chosen parameters: 68479088

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 50 summaries

Database :

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1: gb_est1.*

2: gb_est2.*

3: gb_est3.*

4: gb_est4.*

5: gb_est5.*

6: gb_est6.*

7: gb_est7.*

8: gb_est8.*

9: gb_est9.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	16.4	82.0	700	1	AL509140
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3	16.4	82.0	786	9	CL666247
4	16.4	82.0	847	9	CL670484
5	15.6	78.0	362	6	BY667438
6	15.6	78.0	434	5	BY461297
7	15.6	78.0	613	2	BB651761
8	15.4	77.0	214	2	BB216706
9	15.4	77.0	452	7	CK326609
10	15.4	77.0	504	9	CE239112
11	15.4	77.0	756	9	AG593385
12	15.4	77.0	853	6	CD751046
13	15.4	77.0	877	2	BF623577
14	15.4	77.0	953	7	CF455917
15	15.4	77.0	1070	7	CF455948
16	15.4	77.0	1083	5	BQ881573
17	15.4	77.0	1115	4	BG477774
18	15.2	76.0	296	2	BF551618
19	15.2	76.0	432	9	CL214740
20	15.2	76.0	583	5	BU702144
21	15.2	76.0	599	7	CF892278
22	15.2	76.0	608	9	CC875829
23	15.2	76.0	624	7	CF727912
24	15.2	76.0	626	7	CF894749

C 25	15.2	76.0	667	7	CN702732	E0465H10-
26	15.2	76.0	676	7	CF741585	UI-M-HB0-
27	15.2	76.0	682	7	CO429861	UI-M-HX0-
C 28	15.2	76.0	695	6	CA242359	SCEPPL308
C 29	15.2	76.0	695	6	CE362742	tigr-g88-
30	15.2	76.0	712	5	EX083115	EX083115
31	15.2	76.0	727	7	CK634748	UI-M-HD0-
32	15.2	76.0	732	7	CF729144	UI-M-HD0-
33	15.2	76.0	737	6	CA511803	UI-R-FJ0-
34	15.2	76.0	776	7	CK635827	UI-M-HN0-
C 35	15.2	76.0	784	9	AG275475	Cyanidlos
C 36	15.2	76.0	895	4	BI952340	HVSMEM000
C 37	15.2	76.0	1263	5	BU588111	AGENCOURT
38	15.2	76.0	2095	2	BF302952	602030852
39	15.2	76.0	4479	3	AK049209	Mus muscu
C 40	14.8	74.0	184	1	AI715375	UI-R-Y0-a
C 41	14.8	74.0	184	5	BQ303624	QV2-BT063
42	14.8	74.0	194	8	BZ694126	SP-Ba004
43	14.8	74.0	211	2	BE486215	174013 BA
44	14.8	74.0	235	7	CV325892	CM4-MT023
C 45	14.8	74.0	239	5	BX633989	BX633989
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C 47	14.8	74.0	258	1	AA321284	EST23748
C 48	14.8	74.0	300	2	BE401766	CNW02EL08
C 49	14.8	74.0	313	8	BZ943315	CH240 81K
C 50	14.8	74.0	335	6	CB108935	K-EST0149

ALIGNMENTS

AL509140 700 bp mRNA linear EST 04-JAN-2001
AL509140 Hordeum vulgare Barke developing caryopsis (3.-15.DAP)
Hordeum vulgare subsp. vulgare cDNA clone HY10N07V 5', mRNA
sequence.
AL509140 GI:12035643
EST.
Hordeum vulgare subsp. vulgare
Hordeum vulgare subsp. vulgare
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Poideae; Triticeae; Hordeum.
1 (bases 1 to 700)
Michalek, W., Weschke, W., Pleissner, K.-P. and Graner, A.
EST sequencing and analysis in barley
Unpublished (2000)
Contact: Michalek W
Institute for Plant Genetics and Crop Plant Research
Corrensstr.3, D-06466 Gatersleben, Germany
Email: michalek@ipk-gatersleben.de, http://pgrc.ipk-gatersleben.de
Seq primer: T3 primer for 5' end.
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Location/Qualifiers
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/mol_type="mRNA"
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/db_xref="taxon:112509"
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/tissue_type="developing caryopsis (3.-15.DAP)"
/lab_host="XLOLR"
/clone_lib="Hordeum vulgare Barke developing caryopsis (3.-15.DAP)"
/note="Vector: plasmid pBK-CMV; Site 1: EcoRI; Site 2: XhoI; mRNA was made from developing caryopsis (3.-15.DAP) of spring barley variety 'Barke', a high quality malting variety. Cloning sites: EcoRI (5'-end of cDNA) and XhoI (3'-end of cDNA). NOTE: Due to a cloning artefact caused by the kit, in most cases the EcoRI site is NOT present, as well as the EcoRI adapter. Average insert size is 1 kb

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OM nucleic - nucleic search, using sw model

Run on: June 1, 2005, 23:14:35 ; Search time 157.531 Seconds
(without alignments)
6151.841 Million cell updates/sec

Title: US-10-088-117A-22

Perfect score: 20

Sequence: 1 atcarrccnswvgcggtgcc 20

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 4708233 seqs, 24227607955 residues

Total number of hits satisfying chosen parameters: 9416466

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 50 summaries

Database :

1: gb_ba.*
2: gb_hcg.*
3: gb_in.*
4: gb_om.*
5: gb_ov.*
6: gb_pat.*
7: gb_ph.*
8: gb_pl.*
9: gb_pr.*
10: gb_ro.*
11: gb_sts.*
12: gb_sy.*
13: gb_un.*
14: gb_vi.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	16.6	83.0	20	6	AX098625 Sequence
2	16.6	83.0	2292	1	RSU25037
3	16.6	83.0	2475	6	AX098610 Sequence
4	16.6	83.0	2486	6	AX098605 Sequence
5	16.6	83.0	2487	6	AX098604 Sequence
6	16.6	83.0	2487	6	AX098606 Sequence
7	16.6	83.0	2490	1	SFU5974
8	16.6	83.0	2523	6	AX098609 Sequence
9	16.6	83.0	2540	1	RCDSYNG
10	16.6	83.0	2544	6	AX098612 Sequence
11	16.6	83.0	2750	1	RCADRA
12	16.6	83.0	3316	1	RCADMS
13	16.6	83.0	4680	1	ECTOR
14	16.6	83.0	5637	1	RCU49506
15	16.6	83.0	6915	1	SNA6085
16	16.6	83.0	7990	1	AF016236
17	16.6	83.0	10726	1	AE015567
18	16.6	83.0	11289	1	AE005293
19	16.6	83.0	13067	1	AE015128

c 20	16.6	83.0	18252	1	D9Q737
c 21	16.6	83.0	19650	1	D90736
c 22	16.6	83.0	110000	1	U00096.10
c 23	16.6	83.0	214911	2	AC010537
c 24	16.6	83.0	292504	1	AE016981
c 25	16.6	83.0	301276	1	AE016758
c 26	16.6	83.0	302650	1	AP005958
c 27	16.6	83.0	327773	1	AP002554
c 28	15.8	79.0	477	6	AX098613
c 29	15.8	79.0	22418	1	AE008878
c 30	15.8	79.0	56593	9	AL445215
c 31	15.8	79.0	245050	1	AL627280
c 32	15.8	79.0	300592	1	AE016846
c 33	15.6	78.0	201	11	BV200860
c 34	15.6	78.0	201	11	BV200998
c 35	15.6	78.0	303	6	BD135671
c 36	15.6	78.0	376	6	AX321171
c 37	15.6	78.0	411	6	BD180449
c 38	15.6	78.0	414	1	AB107688
c 39	15.6	78.0	445	6	AX885383
c 40	15.6	78.0	445	6	BD024993
c 41	15.6	78.0	459	9	BT007045
c 42	15.6	78.0	459	9	CR541718
c 43	15.6	78.0	459	12	AX335665
c 44	15.6	78.0	459	12	BT007776
c 45	15.6	78.0	501	6	AX321130
c 46	15.6	78.0	501	6	AX321420
c 47	15.6	78.0	518	6	AX381591
c 48	15.6	78.0	599	6	AX321189
c 49	15.6	78.0	638	5	AF043542
c 50	15.6	78.0	647	6	BD079935

ALIGNMENTS

RESULT 1
AX098625
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL
FEATURES
ORIGIN

AX098625
Sequence 22 from Patent WO0120030.
AX098625
AX098625.1 GI:13537886
synthetic construct
synthetic construct
other sequences; artificial sequences.
1
Giordano,G., dos Santos,J.P. and Mejean,V.
Nucleotide sequences derived from genes coding for trimethylamine
n-oxide reductase, uses thereof in particular for detecting
bacteria
Patent: WO 0120030-A 22 22-MAR-2001;
CENTRE NATIONAL DE LA RECHERCHE SCIENTIFIQUE (CNRS) (FR)
Location/Qualifiers
1..20
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/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="amorce PCR"

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Best Local Similarity 100.0%; Pred. No. 2.6e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ATCARRCCNSWVGCGTGC 20
|||||
Db 1 ATCARRCCNSWVGCGTGC 20

RESULT 2
RSU25037/c
LOCUS
RSU25037
2292 bp DNA linear BCT 16-APR-1998

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OM nucleic - nucleic search, using sw model

Run on: June 1, 2005, 22:48:55 ; Search time 19,9769 Seconds
(without alignments)
5946.580 Million cell updates/sec

Title: US-10-088-117A-22

Perfect score: 20

Sequence: 1 atccaricnswvgggtgcc 20

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 4390206 seqs, 2959870667 residues

Total number of hits satisfying chosen parameters: 8780412

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum first 50 summaries
Listing first 50 summaries

Database : N Geneseq 16Dec04:*

- 1: Geneseqn1980a:*
- 2: Geneseqn1990a:*
- 3: Geneseqn2000a:*
- 4: Geneseqn2001a:*
- 5: Geneseqn2001b:*
- 6: Geneseqn2002a:*
- 7: Geneseqn2002b:*
- 8: Geneseqn2003a:*
- 9: Geneseqn2003b:*
- 10: Geneseqn2003c:*
- 11: Geneseqn2003d:*
- 12: Geneseqn2004a:*
- 13: Geneseqn2004b:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	16.6	83.0	20	4 AAF79961	AAF79961 PCR prime
C. 2	16.6	83.0	2475	4 AAF79948	AAF79948 Nucleotid
C. 3	16.6	83.0	2486	4 AAF79944	AAF79944 Nucleotid
C. 4	16.6	83.0	2487	4 AAF79945	AAF79945 Nucleotid
C. 5	16.6	83.0	2487	4 AAF79943	AAF79943 Nucleotid
C. 6	16.6	83.0	2523	4 AAF79947	AAF79947 Nucleotid
C. 7	16.6	83.0	2544	4 AAF79949	AAF79949 Nucleotid
C. 8	16.6	83.0	2547	13 ADS45929	ADS45929 Bacterial
C. 9	16.6	83.0	2853	5 AAF79908	AAF79908 DNA encod
C. 10	16.6	83.0	2853	5 AAF79906	AAF79906 DNA encod
C. 11	16.6	83.0	2853	5 AAF79927	AAF79927 DNA encod
C. 12	16.6	83.0	2853	5 AAF79955	AAF79955 DNA encod
C. 13	16.6	83.0	11275	6 AAF79917	AAF79917 E. coli g
C. 14	15.8	79.0	477	4 AAF79950	AAF79950 Partial n
C. 15	15.6	78.0	303	6 AAF79963	AAF79963 cDNA enco
C. 16	15.6	78.0	376	6 AAF79947	AAF79947 Lung smal
C. 17	15.6	78.0	445	3 AAF79948	AAF79948 Human sec
C. 18	15.6	78.0	501	6 AAF79906	AAF79906 Lung smal
C. 19	15.6	78.0	501	6 AAF79917	AAF79917 Lung smal
C. 20	15.6	78.0	518	6 AAF79959	AAF79959 Human col

21	15.6	78.0	576	13 ADS45929	ADS45929 Bacterial
22	15.6	78.0	599	6 AAF79961	AAF79961 Lung smal
23	15.6	78.0	647	2 AAF79901	AAF79901 Gene enco
24	15.6	78.0	670	3 AAF79915	AAF79915 Human nm2
25	15.6	78.0	670	6 AAF79915	AAF79915 cDNA enco
26	15.6	78.0	670	6 AAF79922	AAF79922 Human NM2
27	15.6	78.0	670	8 AAF79980	AAF79980 Gene diff
28	15.6	78.0	670	10 AAF79964	AAF79964 Human chr
29	15.6	78.0	670	12 AAF79909	AAF79909 Human nm2
30	15.6	78.0	670	13 AAF79919	AAF79919 Breast ca
31	15.6	78.0	670	13 AAF79929	AAF79929 Tumour-as
32	15.6	78.0	670	13 AAF79929	AAF79929 Tumour-as
33	15.6	78.0	670	13 AAF79929	AAF79929 Tumour-as
34	15.6	78.0	670	13 AAF79929	AAF79929 Tumour-as
35	15.6	78.0	670	13 AAF79929	AAF79929 Tumour-as
36	15.6	78.0	670	13 AAF79929	AAF79929 Tumour-as
37	15.6	78.0	670	13 AAF79929	AAF79929 Tumour-as
38	15.6	78.0	670	13 AAF79929	AAF79929 Tumour-as
39	15.6	78.0	670	13 AAF79929	AAF79929 Tumour-as
40	15.4	77.0	256	6 AAF79929	AAF79929 Tumour-as
41	15	75.0	573	8 AAF79960	AAF79960 Prokaryot
42	15	75.0	1284	11 AAF79921	AAF79921 Mouse mRN
43	15	75.0	1431	3 AAF79921	AAF79921 Mouse mRN
44	15	75.0	1437	3 AAF79921	AAF79921 Mouse mRN
45	15	75.0	1944	3 AAF79921	AAF79921 Mouse mRN
46	15	75.0	1950	3 AAF79921	AAF79921 Mouse mRN
47	15	75.0	2466	3 AAF79921	AAF79921 Mouse mRN
48	15	75.0	2493	3 AAF79921	AAF79921 Mouse mRN
49	15	75.0	2547	3 AAF79921	AAF79921 Mouse mRN
50	15	75.0	2550	6 AAF79921	AAF79921 Mouse mRN

ALIGNMENTS

RESULT 1

AAF79961 ID AAF79961 standard; DNA; 20 BP.

AC AAF79961;

DT 11-JUN-2001 (first entry)

DE PCR primer used to amplify trimethylamine N-oxide reductase genes.

KW toxA gene; trimethylamine N-oxide reductase; flesh degradation;

KW spoilage bacteria; fish; crustacean; PCR primer; ss.

OS Synthetic.

FN WO200120030-A2.

PD 22-MAR-2001.

XX 15-SEP-2000; 2000WO-FR002578.

XX 15-SEP-1999; 99FR-00011543.

XX (CNRS) CENT NAT RECH SCI.

XX Giordano G, Dos Santos J, Mejean V;

XX WPI; 2001-244822/25.

XX Detecting bacteria that cause flesh degradation in fish, for testing
XX freshness, comprises using probes or primers based on the trimethylamine
XX N-oxide reductase system.

XX Claim 7; Page 42; 91pp; French.

XX PCR primers AAF79951-66 represent PCR primers used to amplify torA and
XX torC genes. TorA and torC are bacterial proteins of the trimethylamine N-
XX oxide reductase system. TorA nucleic acids are used for detecting, in a

Result No.	Query			DB	ID	Description
	Score	Match	Length			
C 1	15.8	79.0	601	4	US-09-949-016-145811	Sequence 145811,
C 2	15.8	79.0	601	4	US-09-949-016-146079	Sequence 146079,
C 3	15.8	79.0	601	4	US-09-949-016-146347	Sequence 146347,
C 4	15.8	79.0	205044	4	US-09-949-016-158511	Sequence 15851, A
C 5	15.8	79.0	205044	4	US-09-949-016-158521	Sequence 15852, A
C 6	15.8	79.0	205044	4	US-09-949-016-158531	Sequence 15853, A
C 7	15.8	79.0	223471	4	US-09-949-016-123871	Sequence 12387, A
C 8	15.8	78.0	223471	4	US-09-949-016-127241	Sequence 12724, A
C 9	15.8	79.0	223471	4	US-09-949-016-127251	Sequence 12725, A
C 10	15.6	78.0	445	4	US-09-513-999C-1246	Sequence 1246, Ap
C 11	15.6	78.0	670	3	US-09-335-948-3	Sequence 3, Appli
C 12	15.6	78.0	670	3	US-07-806-9328-B	Sequence 4, Appli
C 13	15.6	78.0	4316	4	US-09-949-016-5750	Sequence 5750, Ap
C 14	15.6	78.0	5071	4	US-09-949-016-3631	Sequence 363, App
C 15	15.6	78.0	10302	4	US-09-949-016-17492	Sequence 17492, A
C 16	15	75.0	131332	4	US-09-949-016-15535	Sequence 15535, A
C 17	14.6	73.0	465	4	US-09-107-532A-2346	Sequence 2346, Ap
C 18	14.6	73.0	825	4	US-09-902-540-4480	Sequence 4480, Ap
C 19	14.6	73.0	921	4	US-09-252-991A-2100	Sequence 2100, Ap
C 20	14.6	73.0	1019	3	US-09-183-861-19	Sequence 19, Appl
C 21	14.6	73.0	1019	3	US-09-022-765-19	Sequence 19, Appl
C 22	14.6	73.0	1019	4	US-09-551-974A-19	Sequence 19, Appl
C 23	14.6	73.0	1019	4	US-09-565-501A-19	Sequence 19, Appl
C 24	14.6	73.0	1019	4	US-09-639-206A-19	Sequence 19, Appl
C 25	14.6	73.0	1019	4	US-09-874-923-19	Sequence 19, Appl
C 26	14.6	73.0	1019	4	US-08-798-841-19	Sequence 19, Appl
C 27	14.6	73.0	1026	4	US-09-253-991A-2172	Sequence 2172, Ap

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OM nucleic - nucleic search, using sw model

Run on: June 2, 2005, 16:25:53 ; Search time 21.2846 Seconds
(without alignments)
5776.400 Million cell updates/sec

Title: US-10-088-117A-22

Perfect score: 20

Sequence: 1 atcarrccnswvgcggtgcc 20

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 5706582 seqs, 3073711274 residues

Total number of hits satisfying chosen parameters: 11413164

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 50 summaries

Database : Published Applications NA.*

1:	/cgn2_6/ptodata/2/pubpna/US07_PUBCOMB.seq.*
2:	/cgn2_6/ptodata/2/pubpna/US07_PUBCOMB.seq.*
3:	/cgn2_6/ptodata/2/pubpna/US06_NEW_PUB.seq.*
4:	/cgn2_6/ptodata/2/pubpna/US06_PUBCOMB.seq.*
5:	/cgn2_6/ptodata/2/pubpna/US07_NEW_PUB.seq.*
6:	/cgn2_6/ptodata/2/pubpna/US07_PUBCOMB.seq.*
7:	/cgn2_6/ptodata/2/pubpna/US08_NEW_PUB.seq.*
8:	/cgn2_6/ptodata/2/pubpna/US08_PUBCOMB.seq.*
9:	/cgn2_6/ptodata/2/pubpna/US09A_PUBCOMB.seq.*
10:	/cgn2_6/ptodata/2/pubpna/US09B_PUBCOMB.seq.*
11:	/cgn2_6/ptodata/2/pubpna/US09C_PUBCOMB.seq.*
12:	/cgn2_6/ptodata/2/pubpna/US09_NEW_PUB.seq.*
13:	/cgn2_6/ptodata/2/pubpna/US10A_PUBCOMB.seq.*
14:	/cgn2_6/ptodata/2/pubpna/US10B_PUBCOMB.seq.*
15:	/cgn2_6/ptodata/2/pubpna/US10C_PUBCOMB.seq.*
16:	/cgn2_6/ptodata/2/pubpna/US10D_PUBCOMB.seq.*
17:	/cgn2_6/ptodata/2/pubpna/US10E_PUBCOMB.seq.*
18:	/cgn2_6/ptodata/2/pubpna/US10F_PUBCOMB.seq.*
19:	/cgn2_6/ptodata/2/pubpna/US10_NEW_PUB.seq.*
20:	/cgn2_6/ptodata/2/pubpna/US11_NEW_PUB.seq.*
21:	/cgn2_6/ptodata/2/pubpna/US60_NEW_PUB.seq.*
22:	/cgn2_6/ptodata/2/pubpna/US60_PUBCOMB.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
C 1	16.6	83.0	2547	17 US-10-369-493-24476	Sequence 24476, A
C 2	15.6	83.0	11275	16 US-10-240-689-39	Sequence 39, Appl
C 3	15.6	78.0	376	9 US-09-833-790-188	Sequence 188, Appl
4	15.6	78.0	456	17 US-10-133-628-9	Sequence 9, Appli
5	15.6	78.0	456	17 US-10-133-628-10	Sequence 10, Appl
6	15.6	78.0	501	9 US-09-833-790-147	Sequence 147, Appl
7	15.6	78.0	501	9 US-09-833-790-437	Sequence 437, Appl
8	15.6	78.0	518	9 US-09-919-580-529	Sequence 529, Appl
9	15.6	78.0	576	17 US-10-369-493-24359	Sequence 24359, A
10	15.6	78.0	599	9 US-09-833-790-206	Sequence 206, Appl
11	15.6	78.0	670	15 US-10-171-581-32	Sequence 32, Appl

12	15.6	78.0	670	17 US-10-133-937-49	Sequence 49, Appl
13	15.6	78.0	670	17 US-10-172-118-780	Sequence 780, Appl
14	15.6	78.0	670	17 US-10-159-563-49	Sequence 49, Appl
15	15.6	78.0	670	17 US-10-440-464-89	Sequence 89, Appl
16	15.6	78.0	670	17 US-10-342-887-780	Sequence 780, Appl
17	15.6	78.0	5071	18 US-10-723-860-1220	Sequence 1220, Ad
18	15	75.0	393	15 US-10-156-761-3336	Sequence 3336, Ap
19	15	75.0	573	17 US-10-282-122A-27530	Sequence 27530, A
C 20	15	75.0	974	18 US-10-425-115-121422	Sequence 121422, A
C 21	15	75.0	1284	13 US-10-087-192-560	Sequence 560, App
22	15	75.0	1362	15 US-10-156-761-575	Sequence 575, App
23	15	75.0	1431	10 US-09-899-575-6	Sequence 6, Appli
24	15	75.0	1437	10 US-09-899-575-12	Sequence 12, Appl
25	15	75.0	1944	10 US-09-899-575-7	Sequence 7, Appli
26	15	75.0	1950	10 US-09-899-575-13	Sequence 13, Appl
27	15	75.0	2466	10 US-09-899-575-8	Sequence 8, Appli
28	15	75.0	2493	10 US-09-899-575-14	Sequence 14, Appl
29	15	75.0	2547	10 US-09-899-575-9	Sequence 9, Appli
30	15	75.0	2550	10 US-09-967-464-65	Sequence 65, Appl
31	15	75.0	2562	18 US-10-441-926-3	Sequence 3, Appli
32	15	75.0	2562	18 US-10-441-949-3	Sequence 3, Appli
33	15	75.0	2565	10 US-09-899-575-15	Sequence 15, Appl
34	15	75.0	2565	10 US-09-899-575-97	Sequence 97, Appl
35	15	75.0	2565	15 US-10-130-435-205	Sequence 205, Appl
36	15	75.0	2568	10 US-09-967-464-66	Sequence 66, Appl
C 37	15	75.0	3720	17 US-10-282-122A-40445	Sequence 40445, A
38	15	75.0	32591	17 US-10-085-117-187	Sequence 187, App
39	15	75.0	90256608	18 US-10-470-565-1	Sequence 1, Appli
40	15	75.0	90256608	15 US-10-156-761-1	Sequence 1, Appli
C 41	15	75.0	90256608	15 US-10-156-761-1	Sequence 31975, A
42	14.8	74.0	399	17 US-10-369-493-31975	Sequence 641, App
43	14.8	74.0	404	9 US-09-922-217-641	Sequence 641, App
44	14.8	74.0	404	9 US-09-833-263-641	Sequence 641, App
45	14.8	74.0	404	13 US-10-025-380-641	Sequence 641, App
46	14.8	74.0	612	18 US-10-363-829-100	Sequence 100, App
47	14.6	73.0	405	10 US-09-233-183A-2681	Sequence 2681, Ap
48	14.6	73.0	457	9 US-09-833-790-197	Sequence 197, App
49	14.6	73.0	886	18 US-10-425-115-91080	Sequence 91080, A
50	14.6	73.0	947	17 US-10-424-599-79483	Sequence 79483, A

ALIGNMENTS

RESULT 1
US-10-369-493-24476/c
; Sequence 24476, Application US/10369493
; Publication No. US20030233675A1
; GENERAL INFORMATION:
; APPLICANT: Cao, Yongwei
; APPLICANT: Hinkle, Gregory J.
; APPLICANT: Slater, Steven C.
; APPLICANT: Goldman, Barry S.
; APPLICANT: Chen, Xianfeng
; TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF
; FILE REFERENCE: 38-10(52052)B
; CURRENT APPLICATION NUMBER: US/10/369,493
; PRIOR FILING DATE: 2003-02-28
; PRIOR APPLICATION NUMBER: US 60/360,039
; PRIOR FILING DATE: 2002-02-21
; NUMBER OF SEQ ID NOS: 47374
; SEQ ID NO 24476
; LENGTH: 2547
; TYPE: DNA
; ORGANISM: Escherichia coli
US-10-369-493-24476

Query Match 83.0%; Score 16.6; DB 17; Length 2547;
Best Local Similarity 70.0%; Pred. No. 46;
Matches 14; Conservative 5; Mismatches 1; Indels 0; Gaps 0;

QY 1 ATCARRCCNWSVGGCGTGCC 20

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OM nucleic - nucleic search, using sw model

Run on: June 2, 2005, 07:12:26 ; Search time 134.492 Seconds
(without alignments)
5660.438 Million cell updates/sec

Title: US-10-088-117A-22

Perfect score: 20

Sequence: 1 atcarrccnswvgcgtycc 20

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 34239544 seqs, 19032134700 residues

Total number of hits satisfying chosen parameters: 68479088

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 50 summaries

Database :

EST.*

1: gb_est1.*

2: gb_est2.*

3: gb_hic.*

4: gb_est3.*

5: gb_est4.*

6: gb_est5.*

7: gb_est6.*

8: gb_gss1.*

9: gb_gss2.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
C 1	16.6	83.0	244	1	AV626231
C 2	16.6	83.0	406	5	BP094961
C 3	16.6	83.0	543	2	BE323149
C 4	16.6	83.0	638	7	CF864909
C 5	15.8	79.0	501	7	CK098963
C 6	15.6	78.0	124	1	AA471268
C 7	15.6	78.0	138	6	CD739260
C 8	15.6	78.0	151	6	CD615018
C 9	15.6	78.0	161	6	CD615025
C 10	15.6	78.0	163	6	CB119089
C 11	15.6	78.0	164	6	CD615026
C 12	15.6	78.0	167	6	CD615017
C 13	15.6	78.0	171	6	CD731078
C 14	15.6	78.0	173	6	CB119092
C 15	15.6	78.0	179	4	BM841467
C 16	15.6	78.0	180	6	CD615015
C 17	15.6	78.0	180	6	CD615016
C 18	15.6	78.0	182	6	CD615029
C 19	15.6	78.0	183	6	CD615030
C 20	15.6	78.0	192	2	BE775542
C 21	15.6	78.0	208	6	CD615022
C 22	15.6	78.0	208	7	D56165
C 23	15.6	78.0	214	7	CF644006
C 24	15.6	78.0	221	6	CB122740

25	15.6	78.0	223	2	BP651540
26	15.6	78.0	244	2	AW248343
27	15.6	78.0	245	6	CD615019
C 28	15.6	78.0	245	6	CD615020
29	15.6	78.0	245	7	CF117825
30	15.6	78.0	246	7	CV036728
31	15.6	78.0	257	6	CB121817
32	15.6	78.0	268	5	BE257118
33	15.6	78.0	268	7	CN981851
34	15.6	78.0	273	2	AW418176
35	15.6	78.0	279	6	CB298002
36	15.6	78.0	285	6	CB117146
37	15.6	78.0	285	7	CF116418
38	15.6	78.0	297	2	BE845901
39	15.6	78.0	300	1	AU098718
40	15.6	78.0	302	2	BE227297
C 41	15.6	78.0	302	6	CD615027
42	15.6	78.0	304	6	CD615028
43	15.6	78.0	317	4	BM825665
44	15.6	78.0	317	6	CB113993
45	15.6	78.0	318	7	CK441639
46	15.6	78.0	325	7	CK611857
47	15.6	78.0	326	7	CN221996
48	15.6	78.0	330	7	CK612075
C 49	15.6	78.0	334	7	CV312969
50	15.6	78.0	335	7	CN267145

ALIGNMENTS

RESULT 1
AV626231/c
LOCUS AV626231 Chlamydomonas reinhardtii 5' to 0.04% CO2 Chlamydomonas
DEFINITION reinhardtii cDNA clone LCL004907 r 5', mRNA sequence.
ACCESSION AV626231
VERSION AV626231.1 GI:10788511
KEYWORDS EST.
SOURCE Chlamydomonas reinhardtii
ORGANISM Chlamydomonas reinhardtii
Eukaryota; Viridiplantae; Chlorophyta; Chlorophyceae; Volvocales;
Chlamydomonadaceae; Chlamydomonas.
REFERENCE 1 (bases 1 to 244)
AUTHORS Asamizu, E., Miura, K., Kuchio, K., Inoue, Y., Fukuzawa, H., Ohyama, K., Nakamura, Y. and Tabata, S.
TITLE Generation of expressed sequence tags from low-CO2 and high-CO2 adapted cells of Chlamydomonas reinhardtii
JOURNAL DNA Res. 7 (5), 305-307 (2000)
MEDLINE 20539644
PubMed 11089912
COMMENT Contact: Erika Asamizu
The First Laboratory for Plant Gene Research
Kazusa DNA Research Institute
Yana 1532-3, Kisarazu, Chiba 232-0812, Japan
Email: asamizu@kazusa.or.jp, URL: http://www.kazusa.or.jp/en/plant/.
FEATURES
Location/Qualifiers
1..244
/organism="Chlamydomonas reinhardtii"
/mol_type="mRNA"
/strain="C9"
/db_xref="taxon:3055"
/clone="LCL004907 r"
/note="Vector: pBluescriptII SK-; Site 1: EcoRI; Site 2: XhoI. The cDNA library was constructed from cells cultured in a carbon stress acclimatized condition in which carbon dioxide concentration in the bubbling gas was changed from 5% to 0.04%".

ORIGIN

Query Match 83.0%; Score 16.6; DB 1; Length 244;
Best Local Similarity 70.0%; Pred. No. 5.1e+02;

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: June 1, 2005, 23:14:35 ; Search time 133.901 Seconds
(without alignments)
6151.841 Million cell updates/sec

Title: US-10-088-117A-23

Perfect score: 17

Sequence: 1 gbcaactcdgtytgagg 17

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 4708233 seqs, 24227607955 residues

Total number of hits satisfying chosen parameters: 9416466

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 50 summaries

Database : GenBank:

1: gb_ba:*
2: gb_htg:*
3: gb_in:*
4: gb_om:*
5: gb_ov:*
6: gb_pat:*
7: gb_ph:*
8: gb_pl:*
9: gb_pr:*
10: gb_ro:*
11: gb_sts:*
12: gb_sy:*
13: gb_un:*
14: gb_vl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	14.2	83.5	17	6	AX098626 Sequence
2	14.2	83.5	377	6	AX331490 Sequence
3	14.2	83.5	506	8	AB108334 Phleum pr
4	14.2	83.5	586	6	CQ780984 Sequence
5	14.2	83.5	586	6	BD125693 Primer fo
6	14.2	83.5	738	3	CAU94757
7	14.2	83.5	812	6	BD269304
8	14.2	83.5	812	6	BD276375
9	14.2	83.5	813	9	BC029416
10	14.2	83.5	1075	9	BC020203
11	14.2	83.5	1559	9	AF217989
12	14.2	83.5	2000	6	BD270046
13	14.2	83.5	2146	5	BC078093
14	14.2	83.5	2238	9	AY048054
15	14.2	83.5	2238	9	AY450874
16	14.2	83.5	2261	6	CQ782800
17	14.2	83.5	2261	6	BD127320
18	14.2	83.5	2261	9	AK074848
19	14.2	83.5	2292	1	RSU25037

c 20	14.2	83.5	2424	9	AK098808
c 21	14.2	83.5	2443	6	AR528481
c 22	14.2	83.5	2443	6	AX463924
c 23	14.2	83.5	2443	9	AY358477
c 24	14.2	83.5	2447	6	AX206905
c 25	14.2	83.5	2475	6	AX098610
c 26	14.2	83.5	2486	6	AX098605
c 27	14.2	83.5	2487	6	AX098604
c 28	14.2	83.5	2487	6	AX098606
c 29	14.2	83.5	2490	1	SPU5974
c 30	14.2	83.5	2523	6	AX098609
c 31	14.2	83.5	2540	1	RC08TNORG
c 32	14.2	83.5	2544	6	AX098612
c 33	14.2	83.5	2750	1	RCADSR
c 34	14.2	83.5	2841	6	AX106709
c 35	14.2	83.5	3299	9	BC018771
c 36	14.2	83.5	3316	1	RCADMS
c 37	14.2	83.5	4680	1	ECTOR
c 38	14.2	83.5	5006	10	MMU24171
c 39	14.2	83.5	5637	1	RCU49506
c 40	14.2	83.5	6915	1	SMA6085
c 41	14.2	83.5	7990	1	AF016236
c 42	14.2	83.5	10726	1	AE015567
c 43	14.2	83.5	11034	1	AE004247
c 44	14.2	83.5	11289	1	AE005293
c 45	14.2	83.5	12083	1	AE002012
c 46	14.2	83.5	13067	1	AE015128
c 47	14.2	83.5	18252	1	D90737
c 48	14.2	83.5	19650	1	D90736
c 49	14.2	83.5	31059	9	AC009005
c 50	14.2	83.5	38102	9	AP001047

ALIGNMENTS

RESULT 1
AX098626
LOCUS AX098626 17 bp DNA linear PAT 02-APR-2001
DEFINITION Sequence 23 from Patent WO0120030.
ACCESSION AX098626
VERSION AX098626.1 GI:13537887
KEYWORDS synthetic construct
SOURCE synthetic construct
ORGANISM synthetic construct
REFERENCE 1
AUTHORS other sequences; artificial sequences.
TITLE Giordano, G., dos Santos, J.P. and Mejean, V.
Nucleotide sequences derived from genes coding for trimethylamine
n-oxide reductase, uses thereof in particular for detecting
bacteria

JOURNAL Patent: WO 0120030-A 23 22-MAR-2001;
CENTRE NATIONAL DE LA RECHERCHE SCIENTIFIQUE (CNRS) (FR)
FEATURES
source
1. .17
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="amorce PCR"

ORIGIN
Query Match 83.5%; Score 14.2; DB 6; Length 17;
Best Local Similarity 100.0%; Pred. No. 7e+02; 0; Indels 0; Gaps 0;
Matches 17; Conservative 0; Mismatches 0;
Qy 1 GBCACRTCDGTYTGAG 17
|||||
Db 1 GBCACRTCDGTYTGAG 17
|||||

RESULT 2
AX331490
LOCUS AX331490 377 bp DNA linear PAT 09-JAN-2002

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OM nucleic - nucleic search, using sw model

Run on: June 1, 2005, 22:48:55 ; Search time 16.9804 Seconds
(without alignments)
5926.580 Million cell updates/sec

Title: US-10-088-117A-23
Perfect score: 17
Sequence: 1 gbcartcdgtgtggyg 17

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 4390206 seqs, 2959870667 residues
Total number of hits satisfying chosen parameters: 8780412

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 50 summaries

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2: Geneseq1990a:.*
3: Geneseq2000a:.*
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7: Geneseq2002b:.*
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9: Geneseq2003b:.*
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11: Geneseq2003ds:.*
12: Geneseq2004a:.*
13: Geneseq2004bs:.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
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4	14.2	83.5	481	ACH36846	Ach36846 Human end
5	14.2	83.5	488	ACH34538	Ach34538 Human end
6	14.2	83.5	586	AAK92664	Aak92664 Human cdn
7	14.2	83.5	586	ADL29091	Adl29091 3' end of
8	14.2	83.5	812	AAA87695	Aaa87695 Human sec
9	14.2	83.5	812	AAC99855	Aac99855 Human sec
10	14.2	83.5	1559	AAS97017	Aas97017 DNA encod
11	14.2	83.5	1921	AA575108	Aas75108 DNA encod
12	14.2	83.5	2000	AA23430	Aaa23430 CDNA enco
13	14.2	83.5	2077	AAAC76416	Aac76416 Human ORF
14	14.2	83.5	2261	AAK94291	Aak94291 Human ful
15	14.2	83.5	2261	ADL30907	Adl30907 Full leng
16	14.2	83.5	2366	AAH99489	Aah99489 Human pro
17	14.2	83.5	2403	ADD78297	Add78297 Human CGD
18	14.2	83.5	2443	AA521272	Aas21272 Human cdn
19	14.2	83.5	2443	ACA03631	Aca03631 CDNA enco
20	14.2	83.5	2443	ABX89169	Abx89169 DNA enco

C 21	14.2	83.5	2443	8	ACD41823	Acda1823 Human sec
C 22	14.2	83.5	2443	8	ACA04052	Acda04052 Human cdn
C 23	14.2	83.5	2443	9	ADA45576	Ada45576 Novel hum
C 24	14.2	83.5	2443	9	ADA76007	Ada76007 Human PRO
C 25	14.2	83.5	2443	9	ADA18657	Ada18657 Human PRO
C 26	14.2	83.5	2443	9	ADA61280	Ada61280 Homo sapi
C 27	14.2	83.5	2443	9	ADB19065	Adb19065 Novel hum
C 28	14.2	83.5	2443	9	ADB27606	Adb27606 CDNA enco
C 29	14.2	83.5	2443	9	ADA86085	Ada86085 Novel hum
C 30	14.2	83.5	2443	9	ADB15649	Adb15649 Human PRO
C 31	14.2	83.5	2443	9	ADA47435	Ada47435 Human PRO
C 32	14.2	83.5	2443	9	ADA67230	Ada67230 Human PRO
C 33	14.2	83.5	2443	9	ADB30237	Adb30237 CDNA enco
C 34	14.2	83.5	2443	9	ADA85533	Ada85533 Novel hum
C 35	14.2	83.5	2443	9	ADA96745	Ada96745 Human PRO
C 36	14.2	83.5	2443	9	ADA79049	Ada79049 Human PRO
C 37	14.2	83.5	2443	9	ADA87188	Ada87188 Novel hum
C 38	14.2	83.5	2443	9	ADB16390	Adb16390 Human PRO
C 39	14.2	83.5	2443	9	ADA91482	Ada91482 Novel hum
C 40	14.2	83.5	2443	9	ADB14545	Adb14545 Human PRO
C 41	14.2	83.5	2443	9	ADB18506	Adb18506 Novel hum
C 42	14.2	83.5	2443	9	ADA93721	Ada93721 Human PRO
C 43	14.2	83.5	2443	9	ADB19617	Adb19617 Novel hum
C 44	14.2	83.5	2443	9	ADB12929	Adb12929 Human PRO
C 45	14.2	83.5	2443	9	ACD98452	Ac98452 Novel hum
C 46	14.2	83.5	2443	9	ADA74183	Ada74183 Human PRO
C 47	14.2	83.5	2443	9	ADB24416	Adb24416 Human PRO
C 48	14.2	83.5	2443	9	ADA81940	Ada81940 Human PRO
C 49	14.2	83.5	2443	9	ADA74903	Ada74903 Human PRO
C 50	14.2	83.5	2443	9	ADA84981	Ada84981 Novel hum

ALIGNMENTS

RESULT 1

AA79962 ID AAF79962 standard; DNA; 17 BP.

XX AAF79962;

XX 11-JUN-2001 (first entry)

XX PCR primer used to amplify trimethylamine N-oxide reductase genes.

XX torA gene; trimethylamine N-oxide reductase; flesh degradation;

XX spoilage bacteria; fish; crustacean; PCR primer; ss.

XX Synthetic.

XX WO200120030-A2.

XX 22-MAR-2001.

XX 15-SEP-2000; 2000WO-FR002578.

XX 15-SEP-1999; 99PR-00011543.

XX (CNRS) CENT NAT RECH SCI.

XX Giordano G, Dos Santos J, Mejean V;

XX WPI; 2001-244822/25.

XX Detecting bacteria that cause flesh degradation in fish, for testing
freshness, comprises using probes or primers based on the trimethylamine
N-oxide reductase system.

XX Claim 7; Page 42; 91pp; French.

XX PCR primers AAF79951-66 represent PCR primers used to amplify torA and
torC genes. TorA and torC are bacterial proteins of the trimethylamine N-
oxide reductase system. TorA nucleic acids are used for detecting, in a

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OM nucleic - nucleic search, using sw model

Run on: June 2, 2005, 08:20:11 ; Search time 5.25038 Seconds
(without alignments)
5298.032 Million cell updates/sec

Title: US-10-088-117A-23

Perfect score: 17
Sequence: 1 gbaacrtcdgtygyg 17

Scoring table: IDENTITY NUC
Gapop 10_0 , Gapext 1.0

Searched: 1202784 seqs, 818138359 residues

Total number of hits satisfying chosen parameters: 2405568

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 50 summaries

Database : Issued Patents_NA.*

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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C 3	13.2	77.6	25	1	US-08-458-218-28
C 4	13.2	77.6	25	2	US-08-450-497-28
C 5	13.2	77.6	25	4	US-08-450-482B-28
C 6	13.2	77.6	25	4	US-09-396-196G-54226
C 7	13.2	77.6	143	4	US-09-621-976-14486
C 8	13.2	77.6	348	4	US-09-621-976-17691
C 9	13.2	77.6	417	1	US-09-513-999C-9859
C 10	13.2	77.6	825	1	US-08-173-5108-92
C 11	13.2	77.6	825	1	US-08-458-218-90
C 12	13.2	77.6	825	2	US-08-450-497-92
C 13	13.2	77.6	825	4	US-08-450-482B-92
C 14	13.2	77.6	864	1	US-08-173-5108-94
C 15	13.2	77.6	864	1	US-08-173-5108-96
C 16	13.2	77.6	864	1	US-08-458-218-92
C 17	13.2	77.6	864	1	US-08-458-218-94
C 18	13.2	77.6	864	2	US-08-450-497-94
C 19	13.2	77.6	864	2	US-08-450-497-96
C 20	13.2	77.6	864	4	US-08-450-482B-94
C 21	13.2	77.6	864	4	US-08-450-482B-96
C 22	13.2	77.6	879	4	US-09-328-352-3931
C 23	13.2	77.6	40130	4	US-09-949-016-17275
C 24	13.2	77.6	112239	4	US-09-949-016-13144
C 25	13	76.5	576	4	US-09-765-298A-23
C 26	13	76.5	579	3	US-09-387-341-191
C 27	13	76.5	638	4	US-09-799-451-208

C 28	13	76.5	2403	4	US-09-949-016-5292	Sequence 5292, Ap
C 29	13	76.5	2403	4	US-09-949-016-5293	Sequence 5293, Ap
C 30	13	76.5	11665	4	US-09-949-016-12446	Sequence 12446, A
C 31	13	76.5	11665	4	US-09-949-016-16500	Sequence 16500, A
C 32	13	76.5	13573	4	US-09-949-016-16327	Sequence 16327, A
C 33	13	76.5	51975	4	US-09-949-016-17261	Sequence 17261, A
C 34	13	76.5	76118	4	US-09-949-016-15593	Sequence 15593, A
C 35	13	76.5	112465	4	US-09-949-016-16424	Sequence 16424, A
C 36	13	76.5	119594	4	US-09-949-016-12080	Sequence 12080, A
C 37	13	76.5	113601	4	US-09-949-016-15952	Sequence 15952, A
C 38	13	76.5	130563	4	US-09-949-016-12273	Sequence 12273, A
C 39	13	76.5	131379	4	US-09-949-016-16050	Sequence 16050, A
C 40	12.6	74.1	38	1	US-08-390-850-920	Sequence 920, App
C 41	12.6	74.1	38	1	US-08-435-634-920	Sequence 920, App
C 42	12.6	74.1	38	4	US-09-371-772B-8921	Sequence 8921, Ap
C 43	12.6	74.1	38	4	US-09-371-772B-9385	Sequence 9385, Ap
C 44	12.6	74.1	38	4	US-09-371-772B-12450	Sequence 12450, A
C 45	12.6	74.1	38	4	US-09-371-772B-13188	Sequence 13188, A
C 46	12.6	74.1	225	4	US-09-513-999C-8201	Sequence 8201, Ap
C 47	12.6	74.1	254	4	US-09-976-594-205	Sequence 205, App
C 48	12.6	74.1	290	4	US-09-313-294A-4710	Sequence 4710, Ap
C 49	12.6	74.1	307	4	US-09-513-999C-3005	Sequence 3005, Ap
C 50	12.6	74.1	336	4	US-09-513-999C-8202	Sequence 8202, Ap

ALIGNMENTS

RESULT 1

US-09-799-451-498/c
; Sequence 498, Application US/09799451
; Patent No. 6783969
; GENERAL INFORMATION:
; APPLICANT: Tang, Y. Tom
; APPLICANT: Zhou, Ping
; APPLICANT: Goodrich, Kyle
; APPLICANT: Asundi, Vinod
; APPLICANT: Ren, Feiyan
; APPLICANT: Zhang, Jie
; APPLICANT: Xue, Aidong J.
; APPLICANT: Zhao, Qing A.
; APPLICANT: Wang, Jian-Rui
; APPLICANT: Ma, Yungqing
; APPLICANT: Yamazaki, Victoria
; APPLICANT: Chen, Rui-hong
; APPLICANT: Wang, Zhiwei
; APPLICANT: Wang, Dunrui
; APPLICANT: Yang, Yonghong
; APPLICANT: Wehrman, Tom
; APPLICANT: Ghosh, Reena
; APPLICANT: Dmanac, Radjoje T.
; TITLE OF INVENTION: No. 6783969el Nucleic Acids and
; FILE REFERENCE: Polypeptides
; CURRENT APPLICATION NUMBER: US/09/799,451
; CURRENT FILING DATE: 2001-03-05
; NUMBER OF SEQ ID NOS: 948
; SOFTWARE: pt FL genes Version 2.0
; SEQ ID NO 498
; LENGTH: 2906
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURES:
; NAME/KEY: CDS
; LOCATION: (321)..(1898)
US-09-799-451-498

Query Match 83.5%; Score 14.2; DB 4; Length 2906;
Best Local Similarity 70.6%; Pred. No. 1.6e+02;
Matches 12; Conservative 5; Mismatches 0; Indels 0; Gaps 0;

QY 1 GBAACRTCDGTYGYGG 17
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OM nucleic - nucleic search, using sw model

Run on: June 2, 2005, 16:25:53 ; Search time 18.0919 Seconds
(without alignments)
5776.400 Million cell updates/sec

Title: US-10-088-117A-23

Perfect score: 17

Sequence: 1 gbcactcdgtgtyg99 17

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 5706582 seqs, 3073711274 residues

Total number of hits satisfying chosen parameters: 11413164

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 50 summaries

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7:	/cgm2_6/ptodata/2/pubpna/US08_NEW_PUB.seq:*
8:	/cgm2_6/ptodata/2/pubpna/US08_PUBCOMB.seq:*
9:	/cgm2_6/ptodata/2/pubpna/US09A_PUBCOMB.seq:*
10:	/cgm2_6/ptodata/2/pubpna/US09B_PUBCOMB.seq:*
11:	/cgm2_6/ptodata/2/pubpna/US09C_PUBCOMB.seq:*
12:	/cgm2_6/ptodata/2/pubpna/US09_NEW_PUB.seq:*
13:	/cgm2_6/ptodata/2/pubpna/US10A_PUBCOMB.seq:*
14:	/cgm2_6/ptodata/2/pubpna/US10B_PUBCOMB.seq:*
15:	/cgm2_6/ptodata/2/pubpna/US10C_PUBCOMB.seq:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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4	14.2	83.5	488	10	US-09-918-995-21750
5	14.2	83.5	812	11	US-09-986-480-48
6	14.2	83.5	812	11	US-09-985-153-40
7	14.2	83.5	812	19	US-10-863-332-48
8	14.2	83.5	1559	15	US-10-301-822-170
9	14.2	83.5	2366	17	US-10-296-115-324
10	14.2	83.5	2443	14	US-10-028-072-57
11	14.2	83.5	2443	14	US-10-140-808-57

C 12	14.2	83.5	2443	14	US-10-121-049-57	Sequence 57, Appl
C 13	14.2	83.5	2443	14	US-10-123-904-57	Sequence 57, Appl
C 14	14.2	83.5	2443	14	US-10-140-470-57	Sequence 57, Appl
C 15	14.2	83.5	2443	14	US-10-175-746-57	Sequence 57, Appl
C 16	14.2	83.5	2443	14	US-10-176-918-57	Sequence 57, Appl
C 17	14.2	83.5	2443	14	US-10-176-921-57	Sequence 57, Appl
C 18	14.2	83.5	2443	14	US-10-137-865-57	Sequence 57, Appl
C 19	14.2	83.5	2443	14	US-10-140-474-57	Sequence 57, Appl
C 20	14.2	83.5	2443	14	US-10-142-431-57	Sequence 57, Appl
C 21	14.2	83.5	2443	14	US-10-143-114-57	Sequence 57, Appl
C 22	14.2	83.5	2443	14	US-10-142-419-57	Sequence 57, Appl
C 23	14.2	83.5	2443	14	US-10-123-262-57	Sequence 57, Appl
C 24	14.2	83.5	2443	14	US-10-142-423-57	Sequence 57, Appl
C 25	14.2	83.5	2443	14	US-10-121-050-57	Sequence 57, Appl
C 26	14.2	83.5	2443	14	US-10-141-755-57	Sequence 57, Appl
C 27	14.2	83.5	2443	14	US-10-143-032-57	Sequence 57, Appl
C 28	14.2	83.5	2443	14	US-10-123-108-57	Sequence 57, Appl
C 29	14.2	83.5	2443	14	US-10-123-236-57	Sequence 57, Appl
C 30	14.2	83.5	2443	14	US-10-123-261-57	Sequence 57, Appl
C 31	14.2	83.5	2443	14	US-10-140-921-57	Sequence 57, Appl
C 32	14.2	83.5	2443	14	US-10-140-928-57	Sequence 57, Appl
C 33	14.2	83.5	2443	14	US-10-121-045-57	Sequence 57, Appl
C 34	14.2	83.5	2443	14	US-10-123-293-57	Sequence 57, Appl
C 35	14.2	83.5	2443	14	US-10-123-903-57	Sequence 57, Appl
C 36	14.2	83.5	2443	14	US-10-124-819-57	Sequence 57, Appl
C 37	14.2	83.5	2443	14	US-10-124-822-57	Sequence 57, Appl
C 38	14.2	83.5	2443	14	US-10-140-925-57	Sequence 57, Appl
C 39	14.2	83.5	2443	14	US-10-160-498-57	Sequence 57, Appl
C 40	14.2	83.5	2443	14	US-10-124-824-57	Sequence 57, Appl
C 41	14.2	83.5	2443	14	US-10-127-825A-57	Sequence 57, Appl
C 42	14.2	83.5	2443	14	US-10-127-829A-57	Sequence 57, Appl
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C 45	14.2	83.5	2443	14	US-10-127-835A-57	Sequence 57, Appl
C 46	14.2	83.5	2443	14	US-10-127-901A-57	Sequence 57, Appl
C 47	14.2	83.5	2443	14	US-10-128-693A-57	Sequence 57, Appl
C 48	14.2	83.5	2443	14	US-10-131-813A-57	Sequence 57, Appl
C 49	14.2	83.5	2443	14	US-10-131-823A-57	Sequence 57, Appl
C 50	14.2	83.5	2443	14	US-10-131-824A-57	Sequence 57, Appl

ALIGNMENTS

RESULT 1
US-09-954-531-932
; Sequence 932, Application US/09954531
; Patent No. US20020165180A1
; GENERAL INFORMATION:
; APPLICANT: Weaver, Zoe
; TITLE OF INVENTION: Process for Identifying Anti-Cancer Therapeutic Agents Using C;
; FILE REFERENCE: 689290-77
; CURRENT APPLICATION NUMBER: US/09/954,531
; PRIOR FILING DATE: 2002-05-02
; PRIOR APPLICATION NUMBER: US/60/233,133
; PRIOR FILING DATE: 2000-09-18
; PRIOR APPLICATION NUMBER: US/60/234,009
; PRIOR FILING DATE: 2000-09-20
; PRIOR APPLICATION NUMBER: US/60/234,034
; PRIOR FILING DATE: 2000-09-20
; PRIOR APPLICATION NUMBER: US/60/234,509
; PRIOR FILING DATE: 2000-09-22
; PRIOR APPLICATION NUMBER: US/60/234,567
; PRIOR FILING DATE: 2000-09-22
; NUMBER OF SEQ ID NOS: 1392
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 932
; LENGTH: 377
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model
Run on: June 2, 2005, 07:12:26 ; Search time 114.318 Seconds
(without alignments)
5660.438 Million cell updates/sec

Title: US-10-088-117A-23

Perfect score: 17
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Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 34239544 seqs, 19032134700 residues

Total number of hits satisfying chosen parameters: 68479088

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 50 summaries

Database :

EST:*
1: gb_est1:*
2: gb_est2:*
3: gb_est3:*
4: gb_est4:*
5: gb_est5:*
6: gb_est6:*
7: gb_est7:*
8: gb_est8:*
9: gb_est9:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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3	14.2	83.5	318	2 AW044207	AW044207 wy71d10.x
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5	14.2	83.5	329	7 H87748	H87748 ys74907.s1
6	14.2	83.5	338	2 BF057006	BF057006 7k14d10.x
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9	14.2	83.5	385	1 AI952364	AI952364 wx27g08.x
10	14.2	83.5	391	1 AI952364	AI952364 wx27g08.x
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ALIGNMENTS

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LOCUS
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C00843
ACCESSION C00843.1 GI:1433073
VERSION EST.
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM
REFERENCE 1 (bases 1 to 220)
AUTHORS
TITLE BodyMap: human gene expression database
JOURNAL Unpublished (1995)
COMMENT Contact: Okubo,K.
Institute for Molecular and Cellular Biol
Osaka University
1-3,Yamada-oka, Suita, Osaka Pref. 565, Japan
Tel: 06-877-5111(ex.3315)
Email: kousakuimcb.osaka-u.ac.jp
We are not submitting the same cDNA sequence redundantly to DDBJ
since 1993. For the abundance information of clones with this
sequence in this library and as well as in other 3'-directed
libraries, see 'http://www.imcb.osaka-u.ac.jp/bodymap'. The
sequences of the clones represented by this GS sequences is also
found there.

FEATURES
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/mol_type="mRNA"
/db_xref="taxon:9606"
/dev_stage="adult"
/clone_lib="Human adult (K.Okubo)"
/note="One or more human adult tissue"

ORIGIN
Query Match 83.5%; Score 14.2; DB 6; Length 220;
Best Local Similarity 70.8%; Pred. No. 2.6e+03;
Matches 12; Conservative 5; Mismatches 0; Indels 0; Gaps 0;